

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCAACACCA**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTCCACCAAGGCTCCCTGTGTGGAAGAATTCATCAGCAAGAAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATGGGATCCGGCGTGGGA
 GAACTGGCCCAAGAACTCAAAGAGGCGAGCATTGGGAACCATCGATGGAAAAAATATTTAAATTT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCGCTGTTCTCATGAATTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCGCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAGTCTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCTGGGTCTCGTCTTTGTGTCTCATTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTTTTCAGCATGTTCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAAGAAGTAT
 CACCAATGTTAGGAGTTCAAATAATGATCCCATTAATCAGTCTGAGTATCTACATGGAT
 ACATTAATAATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**AG**
AGTGACTCAGCTTCTGGCTTCTCTGCTACATCAATATCTTGTTTAATGGGCGAGATATGC
 ATTTAAATAGTTTGTACAAGCAGCTTTCGTGAAAGTTAGAAGATAAGAAACATGTCTATCATA
 TTTAAATGTTCCCGTAAATGTGATGCCTCAGGCTGCTCTTTTCTTGGAGAATAAATGCGAT
 AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAAACATAAGTTTTGTGTCATGAGAATGTAAGCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTTCACTGAGTAACATAAAATTTAGCAACCTGTGTTGCATATTTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCTATAAGTGATTGGAGCTTTGGTAAAGGGACAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTAT
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACCAAGTGGTCATTGTTACATTCATT
 GCTGAACTTAAACAAACCTGTTCTCTGAAACAGGCACAGGTGATGCATTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAAATATAGATGTGGTCATGTTGACTTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTTAAACTATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
 AATACAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSATAISRTPVLMNFMMRGSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLSMFPLPPTTVAGATLYSVAMYGGIVLFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGRKK

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GAAGGCTGCGCTCGCTTCCGAATTCCGGTTCGGTACCGACGTCGGCCGGTCTCGCCCTTCGATAC
CGCGCGCTTCGGCGGGCTTCACCTAGACACTACAGTCGGAGCGCGCGCTGTGAGGG
GGTCGGCAGCGGGAGTCGGCGCGCTTGTGCATCTTGGCATCTGGGTCTGGGTCTGGACATGG
ACATTCGGAGAGCTGGTTCAGGAGCACTCCGGCGAFTACGCGCTATTGGTTCGCCCGACCGCTG
CGCGTGGCCCTGGTGGGCAAACTCTGGCCTCATACGCGCGGCTACCTCTCTCTCGGCCGCA
AACCTCTCTCTTATGGTCTAGATTAGATTGGAGGCCAATCACTGCCACTTTATTTCCCTGTGG
CTTCAGGAATAAGTATTTTATTTGGTCAATTTATATTTCTTATATCATGATTTCTACAGCA
CTTCTTGGAGGCTTTTATTTGGGAGGCGACAGCATATTTATCATGCTCCTCTTTAACTG
GATTTGCATCGTGAATTACTGCTTAGCAATGGATATGCAGTTGCTGATGATCTCTCTGATCT
TGTCAGTACTTTATGCTTGGCCCGCACTGAACAGAGACATGATGTATCATTTTGGTTGGA
ACACGATTTAAAGCCGCTATTTAACTCCGTGGTTACTCTTGGATTCAACTATATCATCGGAGG
CTCGGTATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCCTAATGTTCFA
GATACCCCAATGAGCTTTGGGAGGAGAAATTTCTATTCACCACTCAGTTTGTTCACGCTGG
CTGCCAGTTAGGAGAGAGAGGATACAGGATTTGGTGTGCCCGCTGTAGCATAGGCGAGCG
TGCTGTACAGAATTGGCGGAGCGGGAGACAACTGGGGCGAGGGCTTTCGACTTGGAGCC
AGTGAAGGGCGCGCTCGGGCAGCGCTCTCTCAAGCCACATTTCTCCAGTCTGGGTG
CACTTTACAACACTCGGCTTCGGCTAACACTTGGAACTGCCACCACTGAATGTAGTCTTTC
AGTACGAGCAAAAGTTCTTAAATCCGAGAAATAAATAAGTGTTCCAAAGTTTCACGAT
TCTCATCTCAAGTCTCTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATTCGAAAATGAC
TACATTTTTTGGTGCTCTCTCTCTCCCTTTTCGGTCTGAATAAGGGTTTGAGGGGCTCT
AATCTGCTGGCATTTGAGCTGGGGCTGGGTGACCAAAACCTCTCCAAAAGGACCTTATCTCT
TCTTGACACATGCGCTCTCTCCGACTTTTCCCAACCCCCACATTTGCAACTAGAAAAGTTG
CCCATAAAATTGCTCTGCCCTTGACAGGTTCTGTATTATTTGACTTTTGCCAAGGCTGTC
ACAACAATCATATTTACGTTATTTTCCCTTTTGGTGCGAGAATGTTACCAATAGGGGAGA
AAGACAGCCACGGATGAAGCGTTTCTCAGTTTGTGGAATTGCTTCGACTGACATCGGTTGTT
AACCGTTTGGCCATCTTCAGATATTTTATAAAAAAGTACCACTGAGTTTCATGAGGGGCA
CAGATTGGTTATTAATAGATACAGAGGGTTTGGTCTGGGTGTTTGTTCCTGAGCTAAGTGA
TCAAGACTGTAGTGAAGTTGACGTAACTAGGTTAGGTTTAAACATGGGGGAGTGACCCC
TTTGCGTTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT
TAGAGGATCCGATCATGTTGGCTACAGGAGATGCTCTCTTTAGAGAGTCTGGGACTTG
ATTCCTCATTTCAATCTCATCTCGGATATGTTCCATAGTAAAGGAGGAGAGACCCCTATA
CGTTATTTAAATGTCACTTTTTTGCTATGTCGCCGTTTTTGGTCATGTTCAATTAATGT
GAGGAAGGCGAGCTCCTCTCTCGACGATAGATCTTTTTAAAGCTAATGTAGGCACATCTA
AGGGAATAACATGATTAAGTTGAATGGCTTTAGATCATTTTGGGTTTGAGGGTGTTTA
TCTTGGTCAATGAATGTACAAGCTCTGTGAATCAGACAGCTTAAATTTACACAGCTGTTA
TCGTAGTTGGGCTTTTCCATCAGAGCTTGCTCATACAAAGGCTTTGAGGAGCTTTTGA
TGGCTTTCACACAGATTTTATTTATTTAGAGAGGTTTGGAGCAGTTTGTAGAGCCCA
TTTGAGTGGCTGCTACACTTGAAGGCTTGAAGATGACTTCTTTCCCACTCTTAAACAGTGTGAT
TTGAGGAACAGCTGCTTGAAGGCTTGAAGATGACTTCTTTCCCACTCTTAAACAGTGTGAT
TGTTGTTCTATTCAGATATGTATGATGGCAAACTCTCATTTTGAATAGAGTTTGTGTG
TCTTCTCATTTATTTATATGATAAAATAGGTGGGAGAGTGAACCTTAAGTCTTACTGTCA
TGTTTGTGTTCACTGTGCCACATAAAGTTTACTTGTAAATTTTAGAGGCTAATCTACT
CCAATATGTGTCAGCTACACTGTGACAGGCTGGAGACTCATTTGATATGATAAGAATA
TTTTCTCAGTGAAGTACCGGCGACTCTGGTGTAACCTTTACAGTCAAGTCTGCTCGGAG
CAGTCATTTTTCCTAAAGGTTTACAAGTATTTAGAAGCTTTTCAAGTCAGGCAAAATGTTCT
ATGAAGTTATTTCTTTAAACATGGTTAGGAAGCTGTAGAGCTTATTTGATTTTGTCTGGATT
ATGTTTCTGGAATAATTTTACCAAACAAGCTATTTAGTGTTTGACTTGACAGGCAAAACA
TGACAGTGGATCTCTTTTCAAGTAGGAAAATAAAATCCTATTTTGTATAAGGACTCCC
TTTTTGTAAACTAACTCTTTTATGTGTAAAAATGTAAATTAATAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRADQNGGGGRHNWGGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAAGTGGTTG
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
CCTTGTGGCCCAAAGGCCTAACCGGGTCCGCGGTCTGGCCTAGGGATCTTCCCCTGGCC
CCTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGAGAGCATCG
CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
GAAGTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
GGCCTGTGTCCCCTTGTTTTGTATGATGAAGAAGAAAGCAAATGACCTATACAGAGATTC
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGTTACCTCAAAGAAATGGAATT
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAGGC
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
AAAAATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
GACTGCTTAACCGATGGCTCTGATGTGGTCACTGACCTTGAACACGAAGAGATGAAAATCCT
GAGGGAAGTTCTTAGAAAATCAAAAAGGAATATGACCAGGAAGAAGAAAGAGAGAAAA
AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGTGCATAATG
ATAAATCCCAAGGGGATGGTGAACATTTGCACACCCACCCTCAGAAGTTAAATGCATTT
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAGGTCTGAAACTTCCCTCCCTCC
CACAAAAAGGCCTGAAGATTCTTGGCTTAGAGCATGCGAGCATGAAGGACCAATAGCAAAC
TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTCAAATTGTCTTAAAAATAAATTATTTAGTC
CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGLVPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

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FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTCTCTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAGAAC
 AGTGGAAATGGAAAAACAGTGCCTGTAGTCATCTGTAAATAGTCCCTTGTGAACAAGTATAC
 ATTCTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAACAGTATGATTATCTTCCAAGTCTGTGAATGTGCTGCTCAGAAGCTG
 GTGAAGCTAGTTTTCTGTGCTTGTGTCTATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTGGAAGGAATCTCTGATTTCATGAAGTGGTCCATTCTCGCCT
 TTCTTTATTTCTGGATAAAGTATTGATTGTCTTCTATGCTCTGCTATCTTCAACCCAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGCAGAA
 GAGGCGCTAAAGTGGATCCAGTGGGCTTCCCTCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACTTTACAGCAAACTTGGCAGGACGTGGATTTCATCACGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCCTCTTTTCAGAAGTGAGTGTCCCAAGAAAGACAATTG
 TACAGCAAGGAATGGACTTTTCTGAGCTAAATGGAACACCAAGCCAGAGTTTTTCAGTC
 ACATCCGCTTTGGCATGGGCGCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AAATATCTATAATGAAGAGTACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAAACTCTATTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCTTCAGAGGA
 GTAACCGTGATCAGATTAGAAGTGTGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTATTTTTTGAAGTGCATTCAGGGGCTTTTCAGTGGCTTTTCATTCTGAAGTCTCTGGATAA
 CATGTTCCATGTCTTGTAGGGCCAGGTTACCAGTCTATTATACACACAGTGTCTGTCCCTGG
 TCTTTGACTTCAGGGCCTCCCTGGAATTTTTCTTGGAAAGCCCATAGTCCCTCTCTATATA
 TTTATTTATAATGCGCAGCAAGCCTCAAGTTCGGTAATACGCCCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTTGAACCTTATTTTACATTTTCAGTGTGTGTAATATTTATCTTTTCACTTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGCTATATCTAGCTACTCCCTAAATGGTT
 CCATCCAGGCTTAGAGTACCCAAAGGCTAAGAAATTTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTTGGCCTTCAAGCTTCCAAAAAAGTGTGAATAATCATGTTAGCTATAGCTTGTATAT
 ACATACAGATCAATTTGCCAAATATTCACAATCATGTAGTCTAGTTTACATGCTGCAAGT
 CTTCCTCTTTTAAACATTATAAAGCTAGGTTGTCTCTTGAATTTTGGGGCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCTTTCTAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTGGGATGATGATGCTGTGCTAAATATTTTGTGGAAGAACGAGT
 TTCTCAGACACAACATCTCAGAATTTAATTTTTAGAAATTCATGGGAAATTTGATTTTTGT
 AATAATCTTTTGATGTTTTAAACATTGGTTCCTTAGTCACCATAGTTACCCTTGTATTTTA
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGT
 GTCATTACTCTGAATTTATACATTTTGGAGAATAAGAGGGCATTTTTATTTTATAGTTACT
 AATTCAAGCTGTGACTATTTGCAATATCTTTCCAAGAGTTGAAATGCTGGCTCAGCATAC
 CAGATTGTGAGTGAAGCTGATGCCTAGGAAGCTTTTAAAGGGATCCTTTCAAAAGGATCACTT
 AGCAAAACATGTTGACTTTTAACTGATGATGAATATTAATACTCTAAAATAGAAAGACC
 AGTAATATTAAGTCACTTTACAGTGCTACTTACACTTAAAGTGCAATGGTATTTTTCATG
 GTATTTTGCATGCGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAGCAACAAAGTGACTTGTCTCAGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATGTGAATATGAGCTTTATGGTGT
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATAATTTCAATTTGTGATATCCCAATAATATGACTGCTCAAGAAATTG
 GTGGAATTTGTAATTAATAATTTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPNSNCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSASFVALI
 FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESEDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAACAGTGAATGGAA
AAACAGTGTGTAGTCATCCTGTAATATGCTCCTTGTCACCAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCCCTGCCTTTCTTTATTTC
TGGATAACTTGATTGTCTTCTATGTCCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTACAGGATAGTGTGAAGAGGCGTCTAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCCTGCGGGGCAGAGGAGCAT
 CCCGTCACCAAGTCCCAAGCGGCGTGGCCCCGGGGTCATGGCCAAAGGAGAAGGCGCCGAG
 AGCGGCTCCCGGGCGGGGCTGCTACCCACAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACACAGTTGTCTGTTTGAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCCTCAGATCTAC
 CTATTGCA~~TG~~TGGCTCAGGTGGGCCCCCTTCTCTGCCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCGCTGTCATCAGCAAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTCATTGCGCTACTTCCCT
 ATCTGGTTCGTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATTGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACGCCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAACCATACACATGGCACCCTTCCAC
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTTCATGACCACGGCCCATACATCAAACCT
 ATTACTGGCTTCTCTTCCCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGCTCTGTT
 TTGACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATTCCTCATCTGGCAGTGGTTCTTGACCCGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGCGATCAGTGTGGCAGCTGCCCTTCTTAC
 TACCTTGGTCCATGCTGCCTGATGTCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTTCTATGCTCTTCTTACCAGTTTGCCTCTGGAGTGTG
 ACTGGGCATTTCTACCTCAGTCTGGACTTTGACGGGTACAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATGATGAGGAGAGGCGGCGGCAGAAATAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCCCCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGACTCAGGACCTGTCTGCCGGCTTGTGAGCAGCTGGACTCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGGGTGGCCAGGACACTTGTGTGCTCACTGTGGGCGGGCTGCTCTG
 TGGCTCTGCTCCCTCTGCTGCTGTGGGCGCAAGCCCTGGGGCTGCCACTGTGATA
 TGGCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

MWLRWALS L P P S S C L W A E F G M P S Q T P W W A S A S A N P P G P A W A L C P G S S S P R F W P S L P T S S S G
S C P T S H T A R P I G T C F S I A S L K Q W S R V S M F P T R L S P C S S A T E Q T E R D S A T A Y R M T E V L G T V L
G T A I Q Q Q V G Q A D T P C Q D F N S S T V A S Q S A N H T H G T T S H R E T Q K A Y L L A A G V I V C I Y I I C A V
I L I L G V R E Q R E P Y E A Q Q S E P I A Y F R G L R L V M S H G P Y I K L I T G F L F T S L A F M L V E G N F V L F C T
Y T L G F R N E F Q N L L A I M L S A T I T I P I Q W F L T R F G K K T A V Y V G I S S A V P F L I L V A L M E S N L I
I T Y A V A V A A G I S V A A F L P W S M L P D V I D D F H L K Q P H F H G T E P I F F S F Y V F T K F A S G V S L G
I T S L S L D F A G Y Q T R G S Q P E R V K F I T L N M L V T M A P I V L I L L G L L L F K M Y P I D E R R R Q N K K A L
Q A L R D E A S S G C S E T D S T A S I L

[illegible]

FIGURE 13

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTCTTGACCCGGTTTGCCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGCT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTATGTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGCTACTTGAATACTGAGTTGTTTAGG
 ACTTTCATTTGTGGCAAACCTCCAGAAAAACAACCTTTTGTCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAAATCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTGCTATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGATTGGGGAAAGGTTACAGAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI¹FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIAT²IYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGS³LYMFVQTILSYQM⁴QPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWN⁵PEDKGYVLHMITTAAEWSMSFSFFGFFLT⁶YIRDFQKISLRVEANLHGLTLYD
TAPCPINNER⁷TRLLSRDI

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAATACAGCGTCTAATTAATTCTCTGGTTGTTGAAGCAGT
TACCAAGAATCTTCAACCCCTTCCCAA¹AAAGCTAATTGAGTACACGTTCTCTGTTGAGTACA
CGTTCCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAGAGCCCTCAGTTTCCCTCCT
TCAGCCCTTGTAA²TTTGGACATCTGCTGCTTCATATTTTCATACATCTACTGCGAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCATGAGACACTGGTACAGTANC

Figure 1 shows the chemical structures of compounds 1 through 10. The structures are arranged in two columns. The left column contains structures 1, 3, 5, 7, and 9. The right column contains structures 2, 4, 6, 8, and 10. Each structure is a substituted benzene ring with various functional groups and substituents.

FIGURE 17

CCCACGCGTCCGCCCGCCGCTGCGTCCCGGAGTGAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCGCGGCTGCAC
 CTTGCGCTTGTACTTGCTGTGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCTTCGAGAGTACCGGAAGGAGCACCAGGCCACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCC
 TGTGTTGGGCGCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCACTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCCCTCATTAAAAAATTT
 AGTCAGAAACATCTGAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATGATCTGGATTCTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGAATGGA
 TGTGGTCCCTTAAAGCCCTCATGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGATTACATCAGGT
 TTTCAAACCCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTCTAGAAAATGCTGTTTGT
 GGCGGGGCGCGGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 AAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAEI¹RELSEVLREYR
 KEHQAYVFL²LCGAYLYKQGFAIPGSSFLNVL³AGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVS⁴YFPDKVALLQRKVEENRNSLFF⁵FLFLRLFPMTPNWFLNLSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTL⁶SLDALFSWDTVFKLLAIAMVALIPGTLIK⁷KFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTCCGAACGCCAGCTCAGAA
 TAGGAAAATAACTTTGGGATTTTATATTGGAAGAC**CATGG**ATCTTGTCTGCCAACGAGATCAGCA
 TTTATGACAAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGCATG
 TCAGAGAAGGCAATTGAAAAATTATCAGACAGCTGCTGAAAAAGAATGAACCTCAGAGACC
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCTATCTGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTCTGTTTCTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCACCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGT**TAG**GAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEFQRPPQYPLLVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPFAKKYMSENKGVPL
HGGDEDRFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFAKWWRCFFERWFFPPYPWRRPLNRSQMLRELFV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

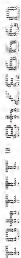


FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGCAGCTGTCCCCGAGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

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FIGURE 22

CCCACGCGTCCGCCCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGT
 CCACTGGTGGCCAGCTGCTAGACCGTGCCATGAGCCGCTGGGGCTGCAGTGGGGACTGCC
 CTCCTTGCCACCCCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTTGCCAA
 CACCAGATGGCGCCATCTACGACAAACAGGTACAGCCAACTTGTCCCAGTTCGAAATG
 GACACGTATGCTAAGAGCCACGACCTTATGTGAGTTTCTGGAATGCCTGCTATGACATGCT
 TATGACAGTGGCAGCGCGCCAGTCAGTGGGAGCGCGCCAGAGTCTGCGGCCCTCCAGGAGG
 TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCCTGGAGGGGTACGCTACACGGCAGTGCTG
 AAGCAGCAGGCAACGCGACACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGT
 CGCCAGCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCGCTGGAACCTGTCCA
 GCGCCGAGACATATTACGCTATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCAGGAGGCG
 CTCACTGCCTCTGGCAGTGACCAAGAGGCCAAAGTGAGCACCCACCCGAGTTGCTGCAGG
 AGGACAGCTCGCGCAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCAGCAGAAGT
 GATGAGCAGCTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGACGGTAGTGCCCGT
 GGTCCCAGGGCTGTGGAGGTCACCAACAGAAATGATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAACCCGAGGAGGGCATCGGCTATGATTTCCGGCGCCCACTGGCCCCAGCTGCGTGAG
 GTCACCTGCGCGCTTTCAACCTGCGCGCTTCAGCACTTGAGCTCTTCTTTATCGATCAGGC
 CAACTACTTCTCAACTTCCCATGCAAGGTGGGACACGCCAGTCTCATCTCCAGCCAGA
 CTCGAGACCCGAGCTGGCCCCATCCCAACCCATACCCAGGTACGGAACACAGGTGTACTCG
 TGCTCTCTGCGCTACGCGCCCTCTCAAGGCTACCTAAGCAGCGCTCCCCCGAGGAGAT
 GCTGCGTGCTCAGGCTTATCCCAAGAAATGGGTACAGCTGAGATATCCAATCTCGAGTACT
 TGATGCAACTCAACACATTGCGGGCGGACCTACAATGACCTGTCTGACTACCTGTGTGTT
 CCCTGGGTCTCTCAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGCGCTCTCCG
 GGACTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAAGAT
 ATGAAGCTTTGAGGATCCAGCAGGAGGACCATGACAAGTCCACTATGGCACCCCACTACTCC
 AATCAGCAGGGGTAGTCAGCACTACTCTCATCCGCGTGGAGCCCTTCACTTCCCTGCACGTCCA
 GCTGCAAGTGGCCGCTTTGACTGCTCCGACCGGAGTTCCACTCGGTGGGGGACGCTGGC
 AGGCAGCCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGAATCTTCTACTTTCTCT
 GACTTCTGGAGAACAGAACGGTTTGTGACTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGTGCTACCCCGTGGGCCAGCTCTCTGAGGACTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCCGGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGCGCTGAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCGAGACTCCCTGTGCACTGCTGAAGGAGCACTCCAACCTAGGCTCTCA
 GCTGAGGAAAGCAACCATCGCCTTGACGCTGGACACTAATCACTAGCATCTTCCAGCA
 CCTGGACCAACTCAAGGCATTCTTCGAGAGGTGACTGTAGTGCCAGTGGGCTGTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTGGGCTCAGCAAAAGACCTCC
 ACCATGGGACGCCAAGACGCGCAGCGACTGCTGAGTGCCCGTGGGTGCCAGGCACTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAGCTGCTATTACGCGCTGGCCACTGGG
 ATGGACGCTCGGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCTTGCACTGGACACCTGTGGCATCTACCTTCATCAGGCTCCCG
 GGACACCACGTGCATGGTGTGGCGGCTCTCTGCATAGGGTGGTGCTAGTAGGCTGGCAC
 CAAAGCTGTGCAAGCTGCTGTATGGGCAATGGGGCTGCAGTGTGACTGTGTGGCATCAGCACT
 GAACCTGACATGGCTGTCTCGGATCTGAGGATGGAATGTGATCATACACACTGATACGCG
 CGGACAGTTTGTAGCGGCACCTACGGCTCTGGGTGCCACATCTCCCTGGACCATTTTCCACC
 TGCACTTGGGCTCCGAGGCGCAGATTGTGGTACAGAGCTCAGGTGGGAGAGCTGCTGGGGCC
 CAGGTACACTCTCTTGCACCTGTATTCAGTCAATGGGAAGTTGGGGCTTCACTGCCCCCT
 GGCAGAGCAGCTCAAGCCCTGACGGTGACAGAGGACTTGTGTGTTGCTGGCAGCCCGCAGT
 GCGCCCTGCACACTCTCCAACTAAACACACTGCTCCCGGCCCGGCTCCCTTGCCCATGGAAG
 GTGGCAATCCGACGCTGGCGCTGACCAAGGAGCGCAGCCAGTGTGTGTGGGCTGGAGGA
 TGGAAGCTCTGCTGGTGTGCTCGCGGGGACGCCCTCTGAGGTGCGCAGCAGCAGTTCGCGC
 GGAAGCTGTGCGGCTGCTGCGGGCGCATCTCCAGGTGTCTCCGGGAGAGCAGGAATACAAC
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGTCTCGGGCGCCGCCCCGCGAGGCGCT
 GCGCGGAGGCGCCCGCCAGAAGTTCGGCGGGAACACCCGGGTGGCAGCCCGAGGCGGTGA
 GCGGGGCCACCTCGCCAGCTCAGGATTTGGCGGGCGATGTTACCCCTCAGGAGTGGGCG
 GCGGGAACCTCCGCCCTGCGCGCTGAGGGCCGCCCTGAGGGCCAGCATGGCGCTT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALET
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLEVTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRENLRSSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQGPPIPHPTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPPTLDSNPAVFRDLSPKIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESADVKELIP
 EFFYFPDFLENQNGFDLGLCLTNEKVGDDVLPWASSPEDFIQQRQALESSEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCYCTYEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSEAAEAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWDSGLRVLTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYILISGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDTGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA
 WERPGAQVTVSYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDGKLVVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTPEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCCCACCTTGTGAACCTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAACTATGGGGTCTGGGGCTCTTC
 TGGACCCCTTAAGTGGGTACTGGCCCTGGGGCAATGCGTCTCGCTGGAGCCTTTGCCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAACTCTGCTTCATCC
 GCACACTCCGTTACCACACTGGGTCAATGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
 ATAGCCCGGTCACTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCCTCTGGTGTCTGGAAAAATTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGCTCTAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTGGAACAAAGTCACAGA
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTTCGGAGGCGTGGGGTCTGTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGCTGCCATCATGACCTCCATCCTGGGGGCTATGTGCATCGCCAGCGGCTCTTTCAGCGT
 TTTCCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCAACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTGAGAGCCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLG
WTLNWLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLFFFGLLVVGGVGLSFFFFSGRIPGLGKDFKSPLHNY
WLPIMTSILGAYVIASGFFSVFGMCDTLFLCFLEDLERNNGLDRPYYSKSLKILGKK
EAPPDNKKRKK

25/330

GAGTCTTGACCGCCGCGGGCTCTTGGTACCTCAGCGCAGCGCAGGCGCTCCGGCCCGCGT
GGCT**ATG**CTTCGTGTCCGATTTCGCCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTTC
CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
CCAGTCAATGTCTCAATGTATACACGATACCCAGATCAAATTACTCATTAACAAGATGA
TGACCTTGAGATTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
GTGGAGCAAACCATGCGGAGGAGGCAGCGCGCAGAGTGGGAGGCCCGGAGAAGAGACATCCT
CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
CTTGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACATACAGAC
CAGTGGGTGCAAGACAAGTCACTCAATGAAATACGCTGACTGATGTGGTGCTCTGCGAGCG
CCACGTTTCCCGCCACAACACCGGACAGGAGTGAAGGAGAACACACTCTCCGTGGACTGCA
CAGGATCTCCTTTGAGTATGAGTCCGCTGGTGTCTTACCAGCACTGGTCCCTCCATGAC
AGCCTGTGCACAACCATGAGTATACCCGAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTC
AGGCCATGGACATCTCCTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAGCACAACTT
TCTGGCCAGCGAGCTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGAGTAACCTGGACAACTG
TACCATGGCCTGGAACCTGCCAAGAGCAGCTGCGAGGCCACCCAGCAGACCATTGCCAGCTGC
CTTTGCCAACCTTCGTGATCTCCCAGGGGCGCTTTCCTGTACTGTCTCTCATGGAGGGCAC
TCCAGATGTGATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
AGTCCCTTGTGTGTTTCGACAAAGAACC GGCGCTGCAAATGCTGCCCCCTGGTGATGGTGCC
CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAGCACCACTCCCGGA
TGCTGCACAACCATTTTGACCTCTAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
CTGGACGCACTTATTTCCCTCTGTCCT**TAG**GAATTTGATCTTCCAGAAATGACCTTCTTATT
TATGTAACCTGGCTTCATTTAGATTGAAGTTATGGACATGAAATTGAGATGTAGAAGCCATT
TTTTATTAAATAAAATGCTTATTTTAGAAA

MFVSDFRKEFFEYVVSQSRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQLETAFA
LEHKEQFHYFILINCGANVDLLDILQPEDTIFVCDSHRPVNVNVYNDTQIKLLIKQDD
LEVPAIEDIFRDEEEDDEHSGNDSGSEPESEKTRLEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSAMVMFELAWMSKDLNDMLWVAIVGLTDQWQDKITQMKYVTDVGVLRH
VSRHNRHNEDEENTLSVDCTRISFEYDLRLVLYQHSWLSHSLCNTSYTAARFKLSVHGQKR
LQEFADMGPLPKQVKQKQFQAMDISLKENLREMIIESANKFGMKMDRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDLSRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGFPLYCSLMEGTPDVMFLSRPASLSLLSKHLLKSFVCSCTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGGAGCGGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAAGTGTGGAGCTAATGTAGACCTATGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC



FIGURE 29

CAGGAACCCCTCTCTTTGGGCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAAAACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAGAGACAGCTTTTTTTGGAAAGCTAA
 GTCTTCCTTTATCGAGTCAAGAAACCCCCCTCTTGAGCTATTTACAGCTTTTAAACAATT
 GAGTAAAGTAGCCTCCGGTCACCATGGTGACAGCCGCTGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTTCTCTGATGTGTGAGATCCGTATGTTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGTGTGACTCTGAGGACCCCTGGATCTGCCCATGTATCTCTCAG
 CCTCTTCTCCGGCCGCCCCACGCCCTGCTGAGATCAGACCCCTACATTAATATCACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCAATGGGCCTGCCAGGGTACATGGGCAGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAAGCCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GGCAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGGCACCGCCAGTTTGTCTGCTCCCTGCTGGCATCTACTTCTCAGCCCTCAATGTGC
 ACAGCTGGAATTACAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTCATC
 CTGTACGCGCAGCCGACGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGGCTCTGGGTGCGGCCTTCAAGCGCCAGCGCGAGAAGCCCATCTACAGCA
 ACGACTTCGACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGG
 CCTCTGGGCCACCCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGCTGCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCTCCGGGACCTGGCATCTTGGGGAGA
 CCTGCTTCTATCTTTGGCTGCCATCATCCCTCCAGCCCTATTCTGCTCCTCTCTTCTCTCT
 TGGACCTATTTTAAAGAGCTTGCTAACCTAAATATCTAGAACCTTCCAGCCCTCGTAGCC
 AGCACTTCTCAAACCTTGGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCT
 GAGTACGAGGTCTGAGTGGGTCCAGGATTCTGTGTTCTCATATGTTCCCTGGGTGATGCTC
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACAGGTTCTAGGACTTCTCAATATTCTAG
 TACTTCTGAACATTCTGGAATCTCTCCACATTCTAGAATTCTCCCAACATTTTTTTTTCT
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCATCTCAGTTTCACTGC
 AACCTCTGCTCCCGGGTTCAGCGATTTCTTCTGCTCAGCCCTCCCTAGTGGCTGGGATTAC
 AGGGCCTGCTACCATGCTGGCTAAATTTTTGTATTTTTAGTAGAGATGGGGTTTACCATA
 TTTGCCAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCACCCGCTCGGCCCTCAAAT
 GCTGGGATTACAGGTGTAGCCACCGCTGCTGGCCAATTCCAACATTCTTAAATCTCTCAT
 CCTCCAGGGCTCCCGTGTGATGTTCTCTTTACCCCTTCCCTCTCTCTTGTCTCAGGGC
 TGCACCATGCAAGCCACCGTTTATTTATTCATTCAAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGGAAGGTGAGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTGACTGGCCA
 GTCCAGCCAGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTGTTTCAGGTGCTGCTGCTGCTTCCCTATACCCACTGCTCCCCAGGCTGG
 TGGGACGGGTCCCGCTGGCAGGGGCAAGTATCTCCTCCCGTTCTCATCCACTGCCGAC
 TGCTCATGTTACAGCAAAACCCAGGGGCTTGGCCAGGTCAAGGGTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGCATTTTGGGGGTGAAGTGGCCCCGGAAGTGAAGACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCTCGGAGAAGACCTGCCCTCTCAGCTGGGATCCC
 CTCTCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGTCTCAGTCCCTTCCACCAAGGTCTATCT
 GAACTTCGTTTCTCCAGAGCTTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCTCATGCCCCCTCACCAGGCTGAGTCCCGGACTCTCAGGCTTTATCAAGGTT
 CTAAGGCCCGGTGGGCTCTCTGCTCTCAGAGCCCTCCTCGGGCTGGTGTGCTGCTTTAC
 AAACACTGTCAGGAGAGGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAGGAGGGACCTCAGGCCCTCCGTTCTTCTTCCAGGGTGGGGTGGCTGTGT
 GTTCCCCAGCTTCAAAACCCAGGTGGCTGCCCTTCTCTCCAGAGGGAGGGCGGCTGCC
 CCATTGGTGTCTATGCAGACTCTGGGCTGAGGTGCCCGGGGGTGTATCTTGTGTCTCAC
 AGCCGAGGGAGCGGTGGCTCATGGCCAGATGACGGAACAGGCTGTGACCAAGTGCAGGA
 AGACCTGTGCTATAAACCCCTGCTGATCTGCCCTGCTGACCCGCCACGCGCTGGC
 GTCCAGCATGATTAAAGATGCTGTCTCTTGGAAAAAAGAAAAA

FIGURE 30

MVTAALGPVWAALLLLLMCEIRMVELTFDRAVASGCQRCCDSEDLDPAHVSSASSSSGRPH
ALPEIRPYINITLLKGDKGDPGPMGLPGYMGREGPQGEPGPGQSGKDKGEMSGAPACQKR
FAFSVGRKTALHSGEDFQTLLEFVFNVLGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPFSERSIMSQSVMLDLAYGDRVWRFLKQRQRENAIYSNDFDYIT
FSGHLIKAEVD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

ACTCGAACGCGAGTTGCTTCGGGACCACGAGGACCCCTCGGGCCCGACCCGCCAGGAAGAGCTG
 AGGCCCGCGGCTGCCCGCGCGGCTCCCTTGCGCCGCGCCGCTCCCGGGACGAGAAG**ATG**TG
 CTCACAGGTCCTCTGCTGCTGCGCGCTGCTCTGCTACTGCCCCTGGGGCTGGGTGTCAGG
 GCTGCCCATCCGCTGCCAGTGCAGCGACGCCACAGACAGCTCTTCTGACCTGCCGCCGACGGG
 ACCACGGTGGCCCGAGAGCTGCCAACCCGACACGGTGGGCTGTACGTCTTTGACCAACGCGAT
 CACCATGCTGCAGCGAGCGAGCTTTTGGCGGCTGCCGGGCTTGCAGCTCCTGGAACTGTCAAC
 AGAACCAAGATCGCCAGCTGCCAGCGGGGTCTTTCAGCGACTTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAAACAGGCTGCATGAATCAACATGAGACCTTCCTGGCTCGGGCGGCGG
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCTTCGCATCGACCG
 TCGACGCTCCTGGAGCTCAAGTGCAGGAGCAACAGCTCGGGGCACTGCCCCGCTGCGCT
 TGCCCGGCTGCTGCTGCTGAGCTCAGCCACCAACAGCTCCTGGCCCTGGAGCGCCGAGCT
 CCTGCGACATGCCAACTGGAGGCGGTGCGCGCTGCTGGTGTGCTGGGGCTGCAGCAGCTGGAGC
 AGGGGCTCTTACGCCGCTTGCAGCACTCCAGCACTGGATGTGTCGCAACACAGCTGGAG
 CGAGTGCACTGTGATCCGAGGCTCCGGGGCTGACGCGCTCGGGCTGGCCGCAACAC
 CCGCATTCGCCAGCTCGGCCCGGAGAGCTTGGCGCGCTGGCTGCCCTCGAGGAGCTGGATG
 TGAACAACCTAAGCTCGAGGCCCTGCTGGGACCTCTTCCGGGCTCTTCCCGCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCTGCCCCTGAGCTGGTTGGCCCGCT
 GGTGCGCGAGAGCCAGCTCACTAGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACCTGGCCGGCTGCTCCTGGAGCTTACTAGCCGACTTTGGCTGCCAGCCACACC
 ACCACAGCCAGCTGATGCCACACAGAGGCCGCTGGTGGGGAGCCCAAGCCCTTGCTCTTCTAG
 CTTGGCTCACTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCGCCAGCCGCCCTTCCA
 CTGCCCAACCGACTGTAGGGGCTGTCCCCAGCCCCAGGACTGCCACCCTCCACTGCCTT
 AATGGGGGACATGCCCACTGGGGACAGGCAACCCCTGGCGTCTGTGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGACGAGATGGGCGAGGGGACAGCCGACGCCCTACACAGTCA
 CGCCGAGGCCACACAGCTCCTTGACCTGGGCACTGAGCCGGTGAGCCCAAGCTCCTCTCGCG
 GTGGGGCTGACGCGCTACCTCCAGGGGAGCTCCGTGACGCTCAGGAGCCTCCGTCTACATTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAGCTTGCAGCTGCCCTGCCCTCGCTGCTG
 AGTACAGGTCACCAAGCTCGGCCGCAACGCCAATCTACTCGCTGTGTGTCATGCTTTGGG
 CCGGGCGGGTGGCGGAGGGCGAGGAGGCTCGGGGAGGGCCATACACCCCAAGCGCTGGA
 CTCCAACCACGCCCCAGTCAACCAGGCCGCGAGGGCAACTGCCGCTCCTCATGTGCGCCG
 CCTTGGCCGGGTCTCTGCGCGGCGCTGGCTCGGGTGGGGGACGCTCATGTGTGCGCGG
 GGGCGGGCATGCGACAGCGGCTCAGGCAAAAGGCGAGTGGGGCGAGGGCTGGGCGCT
 GGAATCGAAGGAGTAGAGGTCCTTCTTGAGGCCAGGCCCGAAGGCAACAGAGGCGGCTGGAG
 AGGCCCTGCCAGCGGCTGTAGTGTGAGTGTGCCATCATGGCTTCCAGGGCTTGGCTCT
 CAGTCAACCCTCCACGCAAGGCCCTACATCT**TAAG**CCAGAGAGAGACAGGGCAGCTGGGGCG
 GGCTCTCAGCCAGCTGAGATGGCCAGCCCTCTGCTGTCACACAGCTAAGTCTTCAGTGC
 CAACCTCGGGGATGTGTGACAGAGGCTGTGTACCAACAGCTGGGCGCTTCTCCTCTGGA
 CCTCGGCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAAGCTCCCCAGAAC
 CGAGTGCTTATGAGGACAGTGTCCCGCTGCCCTCCGCAACGTGCAGTCTCTGGGCACGGCG
 GGCCCTGCATGTGCTGTTAAGCATGCTGGGTCCTGCTGGGCTCTCCACTCAGCGGGA
 CCTTGGGGCCGATGAAGGAAGCTCCCGAAGAGACGAGGAGAGCGGGTAGGCGGCTGTG
 TGACTTATGTTTGGCCCGAAGGCAAGGAACAAAAGAACTGAAAGGAAGATCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCATTTATTCTG
 GGAAGATGTTTTTCAAACCTCAGAGCAAGGAAGCTTTGGTTTTTGTAAAGACAACGATGATG
 AAGGCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVPLLLPLLLLLLALGPGVQGCPSCQCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVFEN
 GITMLDAGSFAGLPGLQLLDLSQNQIASLP SGVFQPLANLSNLDLTANRLHEITNETFRGLR
 RLRLYLKGNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
 GILDANVEALRLAGLGLQQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRGLTRLRLAG
 NTRIAQLRPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPFNCVPLSWFG
 FVWRESHVTLASFEETRCHFPFKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
 SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGTRHHLACLCPE
 GFTGLYCESQMGQGT RPSPTPVTPRPPRSLT LGIEFVSPTS LRVGLQRYLQ GSSVQLRSLRL
 TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPA
 VHSNHAPVTQAREGNPLLIAPALAAVLLAALA AVGAAYCVRGRAMAAAAQDKQVGPAGAG
 PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSP L HAKPYI

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FIGURE 33

GAATCATCCACGCACTGCACTGCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTATATGAGGAAATAAGTGGTAAAAATCCTTGGAAATACAATGAGACTCATCAG
 AAAACATTTACATATTTTGTAGTATTTGTTATGACAGCAGAGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACTGATGACCAACTGCTCCAACATGCTCTAAGAAAGAGTTCCCGCAGACTTG
 ACCCCAGCCACAACGACACTGGATTTATCCTATAACCTCCCTTTTCAACTCCAGAGTTTCAGA
 TTTCTCAATCTGCTCCAAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCACACGCTGG
 ATTTCAAAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTTAATAACAGACTG
 AAGAGTGTAACTTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 TGTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTC
 TTCTTAGAGATTCAGAACTCTTCCTCATTTATGAAGAAGGTAGCCTGCCATCTTAAACACAAC
 AAAACTGCACATTTGTTTTACCAATGGACACAATTTCTGGGTTCTTTTGGGTGATGGAATCA
 AGACTTCAAAAATATTAGAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTAGAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCCTTATCTTACAATTTGTTTGGCATACATCAGTGGAAACACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC
 TCAAAATACTGTAATGAGAATATAAAATGGAGCATGTACATTTAGAGTGTTTTACATTCA
 ACAGGATAAAATCTATTTGCTTTTGACCAAAATGGACATAGAAAACTGACAAATATCAAAATG
 CACAAATGGACACATGCTTTTCCGAAATATCCTACGAAATTTCCAAATTTTAAATTTTGGC
 AATTAATATCTTCAACAGACGAGTTGTTTAAAGAATCTCCAAGCTGCCACTTGAAAACTCT
 CATTTTGAATGGCAATAAATCGAGACACTTTCTTTAGTAAGTGCCTTTGCTAACACACAC
 CCTTGGAACTGTTGATCTGAGTCAAAATCTATTACAACATAAAAAATGATGAAAAATGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTCTACAATAAATTTGTCTGATTTCTGCTTCAG
 GTGCTTGGCCAAAAGTATTCAAATACTTGACCTAAATATAACCAAAATCCAAACTGTACCTA
 AAGAGACTATTCATCTGATGGCCTTACGAGAATTAATATGCATTTAAATTTTCTAAGTAT
 CTCCCTGGATCGAGTCATTTAGTAGACTTTCAGTTCTGAACTATGAAATGAACTTCACTT
 CAGCCCATCTGTGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGGCGGGAAGAA
 ATCCATTCCGGTGTACCTGTGAATTAATAAAATTTTCAATCAGCTTGAACATATTCAGAGGCT
 ATGATGGTTGGATGGTCAGATTCATACACCTGTGAATACCTTTAAACCTAAGGGGAACTAG
 GTTAAAGACGTTTCTCTCCACGAATTTATCTGCAACACAGCTCTGTGTGATTGTCACCAATG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCACAGGGTTAGGAAAACAACCCCA
 AGAACAACTCAAGAGAAATGTCCGATTCACGCAATTTATTTTCAACAGTGAACATGATTTCT
 TGTGGGTGAAGAATGAATGATCCCAATCTAGAGAAGGAAGATGTTTCTATCTTGATTGCT
 CTTTATGAAGACTATTTTCCCTGGCAAAAGCATTAGTGAAAAATCTGATCATATAATCTTATC
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTCTACTTTGGCCACCACAATCTCTCCATGAAAATCTGATCATATAATCTTTATC
 TTACTGGAACCCATTCATTTCTATTGCAATTCACCAAGGATCATATAACTGAAAAGCTCTCCT
 GGAATAAAAAAGCATACTTGAATGGCCCAAGGATAGGCGTAAGTGGGGCTTTTCTGGGGCA
 ACCTTCGAGCTGCTATTAATGTTAATGTATAGGCCACAGAGAAATGTATGAATCGAGACA
 TTCACAGAGTTAAATGAAGAGCTCGAGGGTTCAACATCTCTGATGAGAACAGATTGTCT
 ATAAATCCCACAGTCCATTTGGGAAGTTGGGGACCATACACTGTTGGGATGTACATTGATA
 CAACCTTTATGAGCAATTTTGAACAATTTTATAAATAAAAAATGGTATATTCCTTCATA
 TCAAGTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACACCTTCAAGTTTATAAAG
 GCTTTATGGAATAAAGTGTCTCATCCAGGATTTTATATATCATGAAAAATGTGGCCAGGTGC
 AGTGGCTCACTCTTGTAACTCCAGCATATGGGAGGCCAAGTGGGTGACCCACGAGGTCAA
 GAGATGGAGCCACTTGTGCCAACATGGTGAACCCCTGTCTACTAAAAATACAAAATTA
 GCTGGGCGTGATGGTGCACGCGTGTAGTCCAGCTACTTTGGGAGGCTGAGGCGAGGAAATCG
 CTGGAACCCGGGAGTGGCAGTTGCACTGAGCTGAGATCGAGCCATGCATCCAGCTGGT
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGTGAAGAAACATCC
 TCAATGGCCACAAAATAAGTCTAATTCATAAATATAGTACATTAATGTAAATATATATTA
 CATGCCACTAAAAAGAAATAGGTAGCTGTATATTTCCGGTATGAAAAAACAATATTAATAT
 GTTATAAATATTAGTTGGTGGTCAAAACTAATTTGGTTTGGTCATGAAATGGCATTGAA
 ATAAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTGGGCTCGGGAGGTGGA
 TTACAGGAGGACTTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATTTTGAATGA
 ATCTGTATTTCTTTTATAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHVS KLRLVILCHNRIQQLDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVS YEMQRNLSLENAKTSVLL
LNKVDLLWDDLFILQFVWHTSVEHFFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLT KMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLLQHKNDENC SWPETVVNMNLSYNKLS
DSVFRCLPKSIQILD LNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCLHFDLPWYLRMLGQCTQTWHRV
RKTTEQQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSPNFVQNEWCHYEYFAHNNLFHENS DHIIILILEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

GGGGCTTTCTTGGGCTTTTGTCTTGGAAACATGCTCCCAAGAGACCGGCTTCGAGGGGTGGCGGAAAGG
 GAGGGAGAGAGGAAGGGCGGGGCGGGCCGCTCGCCGCCCGCCGGCGCTCTGCGCGCGCTGTCCGCGCCGCG
 CCGAGCCGAGGACGACCCCGCGGCGGGTCAACACGCGCAGCAGCCGCGCGCTCTCCGCGCCGACGCGCCGT
 CTCGTGTGCCCTGCGCCCTGTGCCCGGTCAGTCTTGCGCCGCGCCGCGCCGCGCGCCGCGCTGTACCTGTAC
 CTTGCCCTTGGGCGGGGCGGAGCAGCAGCATGCTCCGCGCCGGGACCGCTACCCAGCGCTGCCCTGCTGTCT
 CTGCGACGTGACCTGCCCGGGGTGGAGCGCCAGGCGCAGCCCTCGAGGACCGCTGATTTATACGGCAGGAGAT
 CTGGAAGCGGGAGGCTACTACGCGCGCCGAGCCGAGCTCTGAGACCTTCTCTCGCCGCTGCTCGCGGGC
 CGGGGAGGAGGTGGAGCGGCGCGCCGAGGAGCCAGGCGCCCGAAGAGGCGCACAGGCCCAAGAAGCTCGT
 AAGAGGAGGAGTGGCTCGGAGCGGCTCCACAGGCTTAACACAGCAACAAAAGATTATGAGACCAAGAG
 CTCTGAGAAGAGCTCAACATCAGAGTGATCACAGTGTCCGTTGGCGGCTGAGAGTGTTCAGAGAGATTTGCCCATCT
 TTGGTCTGGAACCTTGAATTAACATCAGATTTCAGCTCTGCCGCTCCAGGCTGAAGCGCTATGGCTTGGGGGCA
 TCTCAGGGAGACATCAACATCGAGGGGATTAATGAAATGATTTTATGACGAGCGTGTGGCGCGGAAG
 AATATCACTCAGACGTGGAATGAAGTGGCTCTGCGCGCTGACGAGTACTGCTGTCTCATCTCAAGGA
 GGAACCTGCTCTGCTGATGATCTGGTGAATCTATTAAGTGTCTGTGACGAATGACAGGCCACGTGGGTCT
 ACTTTGAATGAGTCTTGAGACATGATTTTGGGGAACAAGTGAAGAGGAGTCCCTGTTCTTAATGAGCT
 ACCCGTCCCATGTGTGCCCGCTACATCCGATAAACCTCAGTCTGGTTGATATGGGAGACATTCGATGAG
 GAAATGAGATCTGGGTGCCACTGCGAGTCTTAATAATTTATTAACCGCGGAACAGGATGACCCAACTGAT
 GATGACCTGGATTTAAGCACCAATATTAAGAAATGCGCGCACTGTGAAGAAATTTGTAATGAATGTGTCC
 CAATATCACAGAAATTTACAACATTTGAAAAGAACCAACAGGCGCTGAGTCTGTATGCTGTGAGATCTCAGAT
 ACCCTGGGAGACGATGAAGTCTGTGAGCCCAAGTTCCATACATCTGCGGGGCGCCAGGCAATGAGTGTGCTGGC
 CGGGAGTCTGTGCTGTGCTGTGCATTTGTGTGTGTGTCAGGATGCTTGGCGGGAATCGCGCATCTGTCACCT
 GTGGAGGAGACCGGATATCAGTCTCCCTCCCTCACCGGCGGATGGCTACAGAAAGGCTCAGGAAGGGGCT
 CGAGCTGGGAGGCTGTCCCTGGAGCTGAGCACCACTGGAATGATCATCAACAACTTTCTTGATTTA
 AACACGGTCTCTGGGAGCGAGAGATCGAGAGATGTCCCAAGGAAGTTCCCAATCACTAATTTGCAATCCC
 TGAAGTGGTTCTGTGAAATGTGACAGGTGGTCCCGCAAGCAAGACGATCATAGCTGGATGGAATAAATCT
 TTTTGTGCTGGGCGCAACTCTCGAGGCGCGAGCTGTGTGGCGATTCCTCAACGCTGTTGGCTGCCCTCCC
 TGAAAGAGGAGAAACACCCCAACCCCGATGACACGTGCTGGCTGGCTGCCCTACTCTTATGCTCTCAC
 ACACGCGCTCATGACAGACGCGCGGAGGAGGTTGCCACAGGAGGACTTCAGAAGAGGAGGAGGCACTGTCA
 ATGGGGCTCTGTCGACACAGCTCGCTGGAATGTGAAGACTTTGAGTACTCTATCAACAACTGCTTCAAGT
 TCCATCTACGCTGGGCTGTATAAATCCCACTGAGACGACGCTCGCCAGGAGTGGGAGATACCGGGAATCT
 TCTGATCGTTTATGACGAGCAAGTTCATCTGGCATTAAGGCTTTGTGAGAGTTCACTGAAAGAAAGATCC
 CAAAGCGCATATCTCTGTAGAAGATTAACCATGACATCGAACCGCAAGTGGGATTTACTGGCGCCTCT
 CTGAACCTGTGAAGATGTGTGTCAGACAAAGGCGAAGGTTTCACTGATCCACAGAACTGTATGTGTGG
 CATATGACATGGGGGCGACAGGTGTGACTTCACATCTGACAAAACACATGTGCGAGGATCGGAGACATGAG
 AGAATTTGGGAAGCAGCGCTCTCAGCTGCGCAGCGGCGGCTGAAGCTCGGGGCGGAAAGACAGCAGCGGT
GGTGACCCTCTGGGCGCTTGAGACTGTCTGGGACGATGCAAAATTAACCAACCTGGTAGTACTCATATG
 TGACTCATCTACTGTGTTCTCTGTAAATCAAGAGTCTCGGAAGAGGCTGCAATGTGAGCGAGCTCC
 CAAAGAGGAGGCTGGAGGCTGAGGCTGTTTCTTTCTTTCTTCCCTTATCACTAAATTAATCTGGACAGGCA
 CAGAGAAGAACTGATGGAGTGAAGAGACTCAGAACGCAACCTGGGAATCAGAGAGAGAGGAGAGAGGAG
 GAGCTTGTCCGTTCAGAGCTGCTGCTGCATAGAAGAGATTTCTGGTGTCTCCCTGTTTCCGTCGACAGCAGG
 GTTCCACGTGAGTTGCAATTTGCACAGCTAAATTCAGCATTTCCAGATTTCCGAGTGGGCTGCCAAATGTATCA
 TTTGAGATGCTCCAGGCGTCTCAAGAAATGACCAACCTCTCTGGCCCTGGGACATGTCAAGCTTGTGTTGGC
 AGCAGCACTGGAATTTGACATAGGCTCATGCGAATGTCACATCACTGAGGACTTGTGTTGGGCGACAGCA
 TGGAGCTCTGCTCAAAATTTGGGCTCATATAACACCGCCAAAGCTCCTGCTGATCACTGAGCTGAGGCT
 CCCCAGTGGGAGGACGAGGACAGGTCCGACCTCTCTGAAGGGCAGAAATTTAGCTGGATCTCTCTTTTATG
 CTGTAGGACTGGAAAGAGCCAGGAATGGGTGGCTGAAGCCCTCTCTGCTGAGTATGTCCCTGTCTGTGCT
 GAATTGAGTGTCTATGGTTGGGCTCATATCAGCTGGGAGTATTTTGTATGTATGAGATGCAAGATCTCCA
 GATTTAGGCTTAATGATGAAACCTCTAGGATATCTGTGGAGCATCAGTTTGGGAGAGATTTGATTAATTA
 CTCTGAGAGAAAGATATGCTCACTTTTGTAAATGTGCTGCTCATGACTGGGAAAAATGAAAAAATAA
 AATAAAGCAATGTGGTAGACCTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPPYARPEPELETFSPPLP
AGPGEWERRRQEPREPPKRAKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDHS
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRNLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSWKTPQEHTPTPDDHVFRLAYSYST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGINAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVS LPARR
LKLGRKR RRG

FIGURE 37

CTAAGAGGACAAGATGAGGCCGGCCCTCTCATTTTCTCCTAGCCCTTCTGTTCTTCTCCTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTCCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTCGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGCCAGTTGTT
 TTCCAATTTACCCGGCTCCGCGGATGACCGTGGGACCTGCCAGTGCTCTGTTCCCTGCCAGACCCACCTTTTC
 CCGTGGACAGAGTGGAAACGCTTGAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGGAGAAAGACTTTCTAAA
 GTGAGGGAATATGTCCAATTAAATAGTGTGTATGAAAGAAACTGTTAAACCTAACTGTCGGAATGACATCAT
 GGAGAAGATACCATCTTTCTTACACTGAACCTGGACTTCGAGCTGTACAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAGGAGAGTTTGGTGGAGCTCAGAAATGTTGACCAGCTGGAGGTGGAGATAGAAAT
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCCTTGCCATTGCCCGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAGAGTGTGAGGCTCTAAAGATCAAAACACCCCTCTGCTCCACCTCTCCCACTC
 CAGGGAGCTGTGCTCATGGTGGTCTGGTGAACATCAGCAACCCGCTGCTGGTTACAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGCTTGGGTAGGGATTACTCTCCAGCATCCAAACAAAGGACTGTATTTGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTTGCTATTGTATATA
 ATGCTCGAGAGTTGCCGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTGAACAACAACATGTACCTAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCAACCAACAGGATGCTGTGACTCAACTCTCCCTAA
 TGCTGCCATATAATAACCGCTTTTATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGATG
 GATTTGGGGTTATTTATCAACTGAAGCCAGCACTGGTAACATGGTGATTTAGTAACTCAATGACACCCACACT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACCGCTTCAATGGTATGTGGGGTTCT
 GTATGCCACCCGACTATGAACACCAGAAGCAGAAGAGATTTTTACTATTATGACACAAACACAGGGGAAAGAGG
 GCAAACTAGACATTTGATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACATAACCTTTTGACCAGAAA
 CTTTATGTCTATAACGATGGTTACCTTCTGAATATGATCTTTCTGCTTGCAGAGGCCCGCTAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAAATGTTGTTGAAAAAATAGTCTTCTCCACTTACTAGATATCTGCAGGGGTGT
 CTAAAAGTGTGTTCAATTTGCAGCAATGTTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTCTCTTGGGAATCATCTGCCCTCTCAGGCGCATTTTGCAATAAAGTCTGCTAGGGGTGGGA
 TTGTCAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTCACTAGAAGCCTTAAATTA
 GGAATTAAGGAACCTTAAACTCAGTATGGCGTCTAGGGATCTTTGTACAGGAAATATTGCCCAATGACTAGTC
 CTATCCATGTAGCACCACATAATCTTCCATGCCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCCTCGAGGGACCAATCTCCAATTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATCTACATCTGTAAAGTGCTGAGTTTATGGAGAGAGGCCCTTTT
 ATGCATTAATTTGTAGATGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACTGCTTTTCTTTCTCTC
 TGTGTCACCTTACTAAAAGTCAGTAGAATCTTACCTCATAACTCCTTCCAAAGGCAGCTCAGAAGATTAG
 AACCAGACTTACTAACCAATCCACCCCCACCAACCCCTTCTACTGCTACTTTAAAAAAATTAATAGTTT
 CTATGGAACCTGATCAAGATTGAAAAATTAATTTCTTTAATTTCAATTTGGAAGTTTATTTACATGACTCTA
 AGCATATAAGAAATCTGATGGCAATGACAAAGTGCTAGCAATTTGTTATCTAATAAAGACCTTGAGCATA
 GCTGCAACTTATGAGTGTATCAGTTGTCATGTAATTTTGGCTTTGTTTAAAGCTGGAAGCTGTAAAGAAAT
 TAAATTTTAAATTTTCTTCTAGACGAGCTATAGAAAAGCTATTGAGAGTACTAGTTAATCAGTGCAGTAGT
 TGAAGACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTGATGACTTTATCATCTAGTCTTTGTCTATT
 TCTCTGTATGTTCAAGTCTAGTCTATAGGATTGCGAGTTTAAATGCTTTACTCCCCCTTTTAAAAATAATGAT
 TAAATGCTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGDVGPPPIPSPGFSSFPGVDSSSSSFSSSSRSRSSSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVNIISKPSVQNLNWRGFSYLYGAWGRDYSPOHPNKGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQSGTAVYNNMYVNMVNTGNIARVNLTNTIAVTQTLPNAAYNRR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGVLYATRTMNTREEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ



GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCTCCCACCTCCAGGGAGTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGTCTAACTGGAGAGGGTTTTCTTATCTATATGGTGCCTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAGGNATGTATTGGNGGCCCATTTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCCATGGATGATTTAGCTTTGTATATAAATGCTCGAGAGT
CGGGATCACCTTACCGCAAGGTAGTGGTAGGTTACAGGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACTGACC

FIGURE 40

TC CGCAGATAGTAA¹AAATCTCGGAAAGCGGAGAAAGAGCTGTCTCCATCTTGTCTGATAT
CCGCTGCTCTTGTGACGTTGTGCGA²ATGGGGAGGCTCGTGGGGCTGTGCTCCATGCGCGAGT
CGATACCATTGTTTGTGTGGAAGTCGCCCTGTGTTTGCATGCGCGATGCTGCTGTAGGGAAC
AACTCCCATCTGTAACATAGATTGATCTATGCACTTTTCTTGCTTTGGAGTATGTGTAGCTTG
TGTAATTGTGATACCGGAATTGGAAGAACAACTGAATAAGATTCTCGAATTTTGTGAGAACT
AGAAAGGTGTTTGTCCTTTGTAACTTTTGGTGTGCTATAAAGCTGTATCTGTTTGTGCTTT
GGTTTGGCTATGTCTTATCTCTCTCTCTCTCTTACTAATGATCAAAGTAGAAGATAGCAGTGA
TCTCTAGAGCTCGAGTCGACAAATGGAATTTGGTTTCTTTAAATTTGCTGCGCAATTTGCAATTA
TTATTGGGGCAGTTCTTCATTCAGAAAGGAATTTTACAACGTGTGTGGTTTTATGTAGGCAGT
CGAGGTGCGCTTTGTTTTCATCTCTACAACTAGTCTTACTTATTGATTTTGCACATTCAT
GAATGAATCTGGGGTTGAAAAAATGGAAGGAAGGAACCTCGAGATGTGTGGTATGCGAGCCTTT
TATCAGCTACAGCTCGAATTTATCTGCTGTTCTTTAGTTGCTATGCTGCTGTTCCTTGTCTAC
TACACTCATCCAGCCAGGTGTTTCAGAAAACAGCGGCTTCATCAGTGTCAACATGCTCTCTCTG
CGTTGGTGCTTCTGTAATGCTTATACTGCCAAAATCAAGAATCAACAACCAAGATCTGGTT
TGTTACAGTCTTCAGTAATTACAGTCTACAACTGTAATTTGACATGTGCAGCTATGACCAAT
GAACCGAAAACAAATTGCAACCAAGTCTACTAAGCAATAATTTGGCTACAATACAAACAGCAC
TGTCCCAAAGGAAGGGCAGTCAGTCCAGAGCTGGTGCGATGCTCAAGGAATTTAGGACATAATTC
TCTTTTGTGTGTGTTATTTTCCAGCATCGTACATCTCAAACAATAGTCAGGTTAATTAACA
CTGACTCTAACAGGATGAATCTACATTAATAGAAGATGTTGGAGCTAGAAGTGCATGTGATC
ACTCGAGGATGGGACGATGTTCCACGAGCTGTAGATAATGAAGAAGGATGCTGCATTTACA
GTTATTCCTTTTTCATCTGCTTTTCTCGCTCTCACTTTATATCATGATGACCTTACC
AACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAGCTCAGTGGACAGCTGTCTGGGTGAA
AATCTCTTCCAGTTGGATTGGCATCGTGTCTGTA³TTTGGACACTGCTGGCAACCACTTGTC
TTACAAATCTCGTAATTTGAC⁴TGAGTGAGACTCTAGCATGAAGTCCCACTTTGATTTATGTC
TTATTTGAAACAGTATTC⁵CAACTTTTGAAGTGTGTGATGTTTGTGCTTCCCATGTAA
TCTCCAGTGTTCTGGCATGAATTAGATTTATCTGCTTGTATCTTTGTATTTCTTTACCAA
GTGCATGTGATATGTGAAGTAGAATGAATTCGAGAGGAAGTTTATGCAATGTGTGATGAT
TAGTAAAGGTGGCCATTATTTGGGCTTATTTCTGCTCTATAGTTGTGAATGTGAAGAGTAA
ACCAATTTGTTTGCATATTTTAAATATATATAGACATTAAGCTGTTT⁶TAGCAACGATTA
GCAAAATGTATGGCTCGCTTTGGAATATTTGATGTGTTGCTCGGCAGGATATCGAAGAAG
ATGGTTTATTTTAAATTTTAAACAACTCACTTAAGTGGCAGTTGTGCTGAAAATCTTATA
AGGTTT⁷TACCCCTGTACAGGAAATTTACACAGGTGGAGGATGTTTGTGGCAATCTAGCTAGT
TTATGGATGGAGGTGCTGGTACATAATTTGAAATACGAGTAAATATCTCTGCTGAGAG
TGGCCTTTGCCACAATTTGAACTGTGAGTAAAGTGTGTTTGGGAAGATATCATCGGTTAGT
GGAATGTTTGGAACTCTCAAGGATGAGTAAAGTGTGTTGGGCGAGCAGGTAGCTACCCCT
GGTAAATGAGGTGTTGGAGCTTAAGTGGTGAAGTACTT⁸CAGCCAGGAATTCAGACCA
TCTTGCACATGCTGAACCTGTCTATAAAAAATCTGCGCTTGAGCATATGCTCTGTGCT
CAGCATGAGAGGCTAGTAGAATGTCTGAGCCAGGCAAGGTTFCAGTGGACAGCACTCA
CGTCACTGCATCTAGCTGGCAGAGTAAAGCCAAAAAATATATATATTTGAATCAAGG
AGGCAAAATTTTACAGGGAAGGAAGTAAC⁹TCAAACCACTAGGCTTTAGTAGGTACTTAT
ATAAATATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACATGAATACAGACTTAATA
GCTCAGATACCTAATTAGGAATTTCAAGTTGGCAATATATGCACTTCTCTGTACATTTAA
AAATTAATTTCTATCAAAATACATGATTAATGTTTACACCTCATCTGTAATTAATGT
GATGTGGATTTGCTGGTGTCCAGATGACCCATAACAGGTCAGAAGATGATGGAATGTTT
AGAATAAATCTGCTGCTTATAGTATATACACAGTCTCAAAGAGTGTTTAAATAGCTTTTGTAT
TTACTGCATGTAATTAAGAAATATAGATTATTGTAACCTTTCAACCTGAAAATCAAGAGT
ATGAGAGTTTAGTTATTGTATGTGTCAGTGTATGCTAAATGAAGCTTTTAAATCTACAAAT
TCTCTTTTAAAAATATTTAATGTGAATGGAATTAACAATTCAGCTTAATCCCCAACCT
TTATCTGTGTGTAGACATTGATTTCCACAATTTTGAATGGCTGTGTTT¹⁰TACCTCTAAATAA
ATGAATTCAGAGAAAAAATAAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLIIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTYSSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSWIGI
VLYVWTLVAPLVLNRDFD

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GCGAGAAAGAAGCTGCTCCATCTTGTCTGTATCCCGCTGCTTCTTNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGCGTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAAGTGCC
CCGTGTTTGTCTATGCCGATGCTGTCCTAGTGAAACAANTCCACTGTAACTAGATGATCTA
TGCACTTTTCTTGCTTGTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACCTGAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATT
TTGGTTGGCTATAAAGCTGTATACGTTTGAGCTGCTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAAGTGAAGATAGCTAGCTGATGCTTAGCTGACGTGCAGTGACAATGGAT
TTTGGTCTTTTAAATTTGCTGCAGCAATGTCAATTATTATTATTTGGGGC

[illegible]

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAAGTAGATTGATCTATGCACTT
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCTTGTAAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACCTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTGGTATGCAGCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTGCGGCGCGCGCGGCTCTCCAAT
 GGCAAATGTGTGGCTGGAGGCGAGCGCGAGGCTTTCCGCAAGAGCAGTGCAGTGTTCAGACCGGGGCGAG
 TCCTGTGAAGACGATATAAGAAACATTTATTAACGTGTATTACGAGGGGAGCGCCGCGGGGCTGTGCG
 ACTCCCCCGGAGACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAAGAAAGCGGAAAGAGGAGGATCC
 GTCGTTTCCAGCCAAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTATGAGGATGCG
 CCGCTGGTTTGTGTGTAGCCACACACAGCTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTCCAGCTTC
 TGGCGGCTTCCGATCTCTGTTTCACTCTCCGCGGAGGCGAGCAGGAGAGTGTGTGCAATCTGTCCGAGTGC
 AAGAGGGACGAGGGAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCAAAGAGACACAGAT
 CACCAAAAAAGAGCATGCGGCCCGCCGAGCCTCGTGCTGTGCTGCCGCACTGTCTTCCTCTGCTGGG
 TGAAGCTCGGCCCTTCTGTGCGACCAACCGCCTGAAAGGCGAGTTTCAGAGGGACCCGAGGAACATCCGCCCA
 ACATCATCTCGTGTGCTGACGCGACGACAGGATGTGGAGCTGGTTCCATGCAGGTGATGAACAGACCCGCGC
 ATCATGGAGCAGGGCGGGGCGCATCTTCATCAACGCTTGTGTGACCAACACCATGTGCTGCCCTCCAGCTCTCT
 CATCTCTACTCGGAACGTACGTTCCACCAACCAACACCTTACACCAACATGAGAATGTCTCTCGCTCTCTGCG
 AGGCACGACGAGAGCGCACCTTTGCCGTGTACCTCAATGACCTGGCTACCGGACAGCTTTCTTCGGGAAG
 TATCTTAATGAATACAAAGGCTCCTACGTCGCCACCGGCTGGAAGGAGTGGGTCCGACTCCTTAAGAACTCCCG
 CTTTATTAATCATACGCTGTGTGCGAACGGGTGAAAGAGAGACCGGCTCCGACTACTCCAAGGATTACTCA
 CAGACCTCATCAACCATGACAGCTGTAGCTTCTCCGCGAGTCCAAGAGATGATCCCGCGACGCGGAGTCTCT
 ATGCTCATCAGCCATGCAGCCCGCCCAACGCGCTGAGGATTCAGCCCAATATTCAGCGCTTCCCAAGCGC
 ATCTCAGCAGCATCAGCGCGAGCTACAACACGCGCCCAACCCGGACAAACACTGGATCATGGCGTACAGGGGCG
 CCATGAAGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAGAGCGCTTGACAGACCGCTCATGTCCGTGGAC
 GACTCCATGGAGACGATTACAACATGCTGGTTGAGACGGGCGAGCTGGACACACAGTACATGCTATACACCGC
 CGACCAAGCTTACCACATCGGCCGCTTTGGCTGTGAAAGGGAATCCATGCCATATGAGTTTGATCATCGGG
 TCCCGTTCTACGTGAGGGGCCCAACGCTGGAAGCGCGCTGTCTGAATCCCCACATCGTCTCAACATTGACCTG
 GCCCCACCATCTGTGACATTTGAGGCTGGACATACCTCGGATATGAGCGGGAATCCATCTCAAGCTGCT
 GGACCGGAGCGCGCGTGAATCGGTTTCACTTGAAGAAAGAGATGAGGCTCTGGCGGAGCTCCTCTTGTGTGG
 AGAGAGCGAAGCTGCTACACAGAGAGACAATGACAAGGTGGAGCGCCAGGAGGAACTTTCTGCCAAGTAC
 CAGCGTGTGAAGACCTGTGTGACGCTGTGTGAGTACCAGCGCGCTGTGAGCAGCTGGGACAGAAAGTGGCAGTG
 TGTGGAGACCGCACGGGGGAAGCTGAAGCTGCATAAGTGAAGGGGCCCATGCGGCTGGGCGGCGAGCAGCGCC
 TCTCAACCTCTGTGCCAGTACTACGGGCGAGGCGAGCGAGGCTGCACCTGTGACAGCGGGGACTACAAGCTC
 AGCTTGGCCGCGAGCGGAAAAAACTCTTCAAGAAAGATACAAGGCCAGCTATGTCCGAGTGTGCTCCATCCG
 CTCAGTGGCCATCGAGGTGGACGCGAGGTTGACACGCTAGGCTGGGTGATGCCGCCAGCCCCGAAACCTCA
 CCAAGCGGCATCTGCCAGGGGCCCTGAGGACCAAGATGACAAGGATGTGGGGACTTCAGTGGCACTGGAGCG
 CTTCCGCACTCATGCGCCCAACCCATTAAAGTGAACATCGGTGCTACATCTAGAGAACACACAGTCCA
 GTGAGCTGGAACCTGATACAGCTCTGAGGCTCGGAAAGACCAAGCTGCACATCGACACGAGATTTGA
 CCGTGCAGAACCAAAATTAAGAACCTGAGGGAAGTCCGAGGTCACTGAAGAAAGCGGGCAGAGAAATTTGAC
 TGTCAAAATGAGTCACTGACCAACACGACCAAAAGCGCGCTCAAGCAGAGGCTCCAGTGTGACATCTTTGAG
 GAAGGGCTCTCAAGAGAAGGACAAGGTGTGGCTGTTGCGGGACGAGAGGCGCAAGAAACTCCGAGAGCTGC
 TCAAGCGCTGCAGAACACACGACCTGCAGCTGCCAGGCTCAAGGCTTCACTCCACGACACACAGCACTGG
 CAGAGGCGGCTTTCTGACACTGGGCGCTTCTGTGCTGCAACAGCGCCCAACATACACGATGTGTGGTAT
 GAGGACCATCAATGAGACTCAAAATCTCTCTGTGTGAATTCGAGTGAACACACTGGACAGGATGTCTCAACGAGCTACACGTACAG
 ACACAGACCCCTACGAGCTGTGATGAGTGCAGTGAACACACTGGACAGGATGTCTCAACGAGCTACACGTACAG
 CTCTGAGGCTGAGGAGCTGCAGGGTTTCAAGCAGTGTAAACCCCGGACTGCAACATGACCTGGATGGAAG
 AAGCTATGAGCAATACAGGACGTTTCAAGCTGGAAGGTGCCAGAAATGAAGAGACCTTCTTCCAATCACTTGG
 GACACTCTGGGAAGGCTGGGAAGGT**TAA**AAAAACACAGAGGTGGACCTCCAAAACATAGAGGCATCACTTGA
 CTGCAAGCGCAATGAAGAACACTGTGGGTGATTTCCAGCAGACCTGTGCTATTTGGCCAGAGGCGCTGAGAAGCG
 AAGCAGCAGCTCTCATCAACATCAGAGATTGTGGAGGATAACAGCAGGAGCAGAGATTACTTCCAGGAAGTCC
 ATTTTTCCTGCTTTTGGCTTGGATTATACCTCACAGCTGCACAAATGCAATTTTTCGTATCAAAAGTGC
 ACCACTAACCTCCCCAGAGGCTCACAAAGGAAACGAGAGAGAGCGAGGCGAGAGAGATTCTTGGAAATTTCT
 TCCCAAGGGGAAAGTCAATTTGAATTTTAAATCATAGGGGAAAGACGCTCTGTCTTAATCTCTTATCTTCT
 TGTGTTTGTCAAAAGAGGAGTATAAGAGCAGGACAGGAGCAAGCTGGAGAGGCTGAAACAGCTGCAGAGAGCG
 TTTGACAAATGAGTCAGTGAAGACAAAGAGATGACATTTACTGAGCTATAAGCCCTGGTTCCTGTGAAGAAA
 CTGCCTTCATTGTATATGTGTGACTATTACATTGTAATCAACATGGGAATTTAGGGGACCTTAATAAGAAAT
 CCAATTTTCAGGAGGTGTGTGCTCAATTAACGCTCTGTGGCGAGTGTAAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMPHRPVL MVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEFDIRVFFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
YQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDLKYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVGRHLKKRP EECDCCHKISYHTQHKGRCLKHRGSSL
HPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNYWCMTINETHNFLCFEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCGYKQCNPRTNRMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLEWEGWEG

[illegible]

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPHAR

FIGURE 50

GCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTA
 CTACTGGGCCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCCACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAGTAACCC
 ATGGCCTGCACCCTCCTGCAGTGCAGTTGCTGAGGAAGTGCAGAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCTTGAGGGACCTGACTTCCCCTGC
 TCCAGGCCTCTTGTCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGACCA
 GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTTTCACCTGGAAAAAA
 AAAAAAAAAA

MSDLLLLGLIGGLTLLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYDNPMPDPKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVTVATFPYTTILSIWLATRVRHPALDITYIKERKLCAYPRLEIYQEDQIHMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSVSVLEVSPGSRETSAAATLSPGAS
SRGWDGDGTRSEHSYSESAGSGSSFELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCGCGCCCCAGTCATGACCCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAATA
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 54

CCCGGGAACGTGTTCTGCTGCCGACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACAGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCTCATTTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCACATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCAC TAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAATAATAATAATAAATTTAAAAAACCTAAAA

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FIGURE 56

CTGCTGCATCCGGGTGCTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGGCGACACCGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGCTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGG
 GAAAAGCGCAATACATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTATGTTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCTTAACAACAACCAAAAAATCTATTGTGGTATGCACCTTGATTAACTT
 ATAAATGTTAGAGGAACTTTACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
 TGTAATAATAAAGAAATTACAAAAGAAATATGGATTGTCAATGTAAGTATTGTGCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCGGTGG
 TCAAAATCTTCCCTACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACGTGGCTTTGAGGGTCTCCCAAGGGTGAGTGGACGTGTGGAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

TTCTTGGCTAAAATCGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCCAAATCTATTGCTTCCATTGCTGCTGGTGAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCACCACCTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTCGGGTCAAACAGGTG
CTCGCAATTTGGCTTTTCGTTGGTTTATAGATGTTGCCCTTTGGATCTCTGATTGCATCTATGTGG
ATTTCTTTTGGAGGTTATGTTGTCTAAAGAAAAGACATAGTATACCCTGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTGGAGGGCTGTTTTTAAGTTTGGC

TGGACGGACCTGAAAAAAATGTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGATTATCATAGATGCAGNTGTTATTTATCCACCATGAAAGATTTC AACCANTCATACC
ATGCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTC CGAGGTGATAGTTACAGTGAAGGTTGTTGGGTCAAACAGGTGCTCGCATTTTGGCTTTT
CGTGGTCTTAAGATGTTGGCCTTTGGATCTCTGATGTCATCATGTGGATTCTTTTGGAGGTT
ATGTTGCTTAAGAAAAGACATAGTATACCTGGAATGTGTTATTTTCCAGAATGCCCTTC
ATCTTTTTTGGAGGGCTGGTTTTAAGTTTGGCCGCATGAAGANTATATGCGAGTG

FIGURE 60

GGACACCGGGTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

60/330

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

61/330
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTNTTGGCTAAATCGGGGGAGTGAGGCGGCCCGGC GCGG
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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FIGURE 63

CGACGCCGGCGTGA**ATG**TGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCCCCCAGCGCCCTGGTAACCTGACAAGGAGGCCAGGAAGAAGGTTCTCAAAACAAGC
TTTTTCTAGCCAACCAAGTGCCCGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
GCTGGGTGCGAGTGC**AA**TTCTAGCTAAAGCTGGCAAGCGAGTCCCTGGTGCTGGAAACAACAT
ACCAAGGCAGGGGGCTGCTGTCA**AC**TTTGGAAAGAA**AT**GGCCCTGAATTGGACACAGGAAT
CCATTACATTTGGGCGTATGGAAGAGGGCGAGCA**AT**GGCCGTTTATCTTGGACAGATCACTG
AAGGGCAGCTGGACTGGGCTCCCTGTCCCTCTCCTTTTGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAAGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATT**CAGGGCC**CAAGGA
GAAGTTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCTCATGCCATCCTGTGAAATTCCTCCCATTGCCCGTGTT**CAGCT**CCTCGAC
AGGTGTGGGCTGCTGACTCGT**TT**CTCTCCATTCCTTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTG**CAGCAGCTGGGGGCC**CTCTGAGCTCCAGGCAGTACTAGCTACATCTTCCCCA
CTTACCGTGTCA**CCCCCA**ACCACAGTGCCTTTTCCATGCACGGCCTGCTGGTCAACCACTAC
ATGAAAGGAGGCTTTTATCCCGAGGGGTTCCAGTGA**AA**TTGCCTTCCACACCATCCCTGT
GATT**CAGCGGGCTGGGGG**CGCTGCTCCACAAGGCCACTGTGCAGAGTGTGGTGGTGGACT
CAGCTGGGAAGCCTGTGGTGTCA**GTGA**AGAGGGGCATGAGCTGGTGAACATCTATTGC
CCCATCGTGGTCTCAACAGCAGGACTGTTCAACACCTATGAACACCTACTGCGGGGAACCGC
CCGCTGCTG**CAGGTGTGA**AGCAGCAACTGGGGACGGTGCGGCCCGGCTTAGGCATGACCT
CTGTTTTCATCTGCGTGCAGGGCACCAGGAAGACCTGCATCTGCGCTCCACCACTACTAT
GTTTATGATGACACGGACATGGACAGGCGATGGAGCGCTACGCTCCATGCCCCAGGAAGA
GGTGC**GGGAACACATCCCT**CTTCTTCTTCGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCGATTCCAGGCGGGTCCACCATGATC**GTCTCAT**ACCCACTACGATCAGTGGTGGT
GAGGAGTGGCAGGCGGAGTGAAGGGAAAGCGGGCAGTGACATGAGACCTTCA**AAAACTC**
CTTTGTGAAGCCTTATGTCA**GTGGT**CCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCACCAAGTCTTATCTGGCTGCTCCCCAGGTTGCC
TGCTACGGGGCTGACCATGACCTGGGCGCGCTGCACCCCTGTGTGATGGCTCCTTGAGGGC
CCAGAGCCCCATCCCCA**ACCTCTA**CTGCAGAGGCGCAGGATATCTTACCTGTGGACTGGTCG
GGGCGCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCTGAGCGGA**ACTTGT**ACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAA**TTAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGCAGCTATAAAGCACTCTAATTTGGTTCGTAGCTGAAAGAGAGGCTAGT
TTTTAAATCA**CA**AATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGTAT
TCTCATGACGAGCGGCGCTTGATC**ATCCCTC**ACCATGCCTCCTAACTCAGTGATCAAGCGGA
ATATTCCATCTGTGGATGAACCCCTGGCAGTGTGTGAGCTCAACCTGGTGGGTTCAGTTCT
TGCTCTGAGGCTTCTGCTCTCATTT**CATTT**AGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAGGGGAGACTAATGAGGCTTAACTCAAAACCTGGGCGTGGT**TTT**GGTTGGCATCCATA
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCA**GTGGCTCTT**CAGGGGACAGGAAT
GCCTGTGCTGCGCCAGTGTGGTCTGAGGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTAGATGATCATATCCAATT**CATAT**GGAAGTCCCGGCTCTGTCTTCTTCA
TCGGGTTGGCAGCTGGTCTCAATGTGCCAGCAGGAGCTCAGTACCTGAGCCTCAATCAAGC
CTTATCCACCAATACACAGGGAAGGCTGATGCAGGGGAAGGCTGACATCAGGATCAGGGCA
TGGACTGGTAAGATGAATCTTGTCTGGGCTGAAGCAGGCTGCAGGCGACTTCCAGCCAAAGG
CAGCAGAGGGGACAGTGCAGGGAGGTGTGGGTTAAGGAGGGAAGT**CACAT**CAGAAAAGGGA
AAGCCACGGAATGTGTGAAGCCAGAAATGGCA**ATTT**GCAGTTAATTAGCACATGTGAGGG
TTAGACAGGTAGGTGTGAAGCTCAAGCTCAAGGTTTGGAA**AAAT**GACTTTTTCAGTTATGCTTTT
GTATCAGACATACGAAGGTCTCTTTGATGTT**CGT**GTTAATGAACATTAATAAATTTATTG
ATTCCATGCTTTAAAAAAAAAAAAAAAA

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MWLPVLVLLAVLALLVLCVKVYLGFGSSPNPFSEDEVKRPAPLVTDKEARKVKVLQAFSAN
QVPEKLDVVVIGSGFGLAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAII DKYIKLVVSVSGAPHAILKFLPLPVVQLLDRCGLLTRFSFPLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGSSIEIAFHTIPVIQRA
GGAVLTkATVQSVLLDSAGKACGVSVKKGHELvNIYCPiVVSNAglFNTyEHLLPGnARCLP
GVKQQLGTVRPGLGMTSVFIClRGTKEDLHLPSTnNYVvYyDTMDMQAMERYVSMpREEAAEH
IPLlFFAFpSAKDFtWEDrFpGRSTmIMlFYtAYEwFEeWQAElKGKRGSDYETfKNSfVEA
SMsvVLKfLPQLEgKvsvTAGSPLtNQfYLAAPRGACyGADHDlGRlHPCVMASlRQSpI
PNLYLTGDFiFTCGLVsALGALLCSAILKRNLYSLDKLNDLSIRAOKKKN

FIGURE 65

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACC GGGCCCCGAGAGGAGGATGCGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TGGGTTGCTGCTGAGCTTGGCCTCGGCGTCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTCTTGATTGAGAAGATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG
 AGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGAGCCCTGCCACTTCCCTTTTCTTTTCTTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAGCAGATGAAAAGTGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCAT
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGCAGACTGC
 TCTTGGCTTTCTGTATGCCCTCTGGACTTGGTGTTAATTCAGTCAGGCAAAGGCTCTTGTAT
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTT
 TCAGCTTTTCATGATCCAGATTTGCTTGTATTAAGACCAATATTCAGTTGAACTTCTTCAA
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA
 ATTTTCTTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTTAAATTTTCTCTGAGTTGGAATGTGAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAAATTCATGGAGTTATTT
 GTGCAGAAATGACTCCAGAGAGCTCTACTTTCTGTTTTTTACTTTTCATGATTGGCTGTCTTC
 CCATTTATCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTACTTTTCTTTGCTAATTTGGAAGATTAAGTCAATTTTAAATAAA
 ATTTATGTCTAAGATTAATAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 66

MRVRIGLTLLCAVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG
EPCHFPPFLFLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAKRRQMQEAEEM
YQTGMKIILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKQGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTGCCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTCTGG
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTIISPVPEDDADYYCSVGYGFSF

CGCCGCCCGCCCGAGACCGGGCCCGGGGGCCGCGGGCGCGGGATCGCGGCCCGGGGGCGG
CGATGACCGCGGAGCGCAGCGCGGGCGCGGCCCTGACCCCGCGCCGCGCCCTGAGCCG
CCCGCCGAGGATCCCGGACAGGCCGAGATGACCGCGCGGAGGCCCTGTGTGCTGCTCTGCTGCCG
CGCTGCTCTGCGGGGGCTTCCACACGGCCCGCGCCGCCAGGCCGCCAACAGATGGCGAC
AAGGTGCTTCCACCGGAGGTGGCGCGCTGGCGGCATCTGTCGGCTGCAGTGTCAGTTGGA
GGGGGACCCCGCGCCCTGACCATTTGGACCAAGGATGGCGGCACCATCCACAGCGGCTTGA
CGCCCTTCGCGCTGCTGCCGACGGGGCTGAAGGTGAAGCAGGTGGACGGGGAGGATGCGCG
GTGTACGTGTGCAAGGCCAACCAAGGCTTCCGGACCGTGGCGAGCTCAATACACCTCTGTC
CTGGATGACATTTAGCCAGGGAAGGAGAGCTTGGGGCGGCAGAGCTTCTCTGGGGGTCAA
AGGACCGCCCGAGCAGCATGGGACAGCAGCCGGCTTACACAGCGCTCCAAATGAGGCG
CGGGTGATCGCACGGCCGTGGGTAGCTTCGTTCGGCTCAAGTGTGTCGACAGGGGACCC
TCGGCGCGCATCATCGTGGATGAAGAGCAGCACAGGCTTTCAGCGCCCGACAGGCGCGCTGAGC
CAGGAGAAGGAAGTTGACATCTAGCCCTGAAGAACTTCGGCCGGAGGACAGCGGCAAAATAC
ACCTTCGCCCGTGTGCAACCGCGGGCGGCATCAACGCCACCTCAAGGTTGGATGTGATTCG
CGGACCGCGTTTCAAAGCCGTGCTCATAGGACGCAACCCCTGAACACAGCGTGGACTTG
GGGGGACACAGCTCTTCCAGTTCGAAGGTGCGCAGCAGCTGAAGCCGGTGATCCAGTTGGCTG
AAGCGCTGGAGTAGCGCGCGGAGGCGGCCCAACTCCACATCGATGTTGGCGGCGCAAG
GTTTGTGTGTGCTGCCACGGGTGACGTTGGTTCGGCGCGCCAGCGGCTTCTACCTCAATAAGC
TGCTCATACCCGTCCCGCAGGACGATCGGGGATGTACATCTGCTTGGCGGCGCAACCC
ATGGGCTACAGTTCCGACAGGCTTCTCTCACGCTGCTTGGCAGCCAAAACCGCCAGGCGC
ACCTTGTGGCTCTCTCGTCTCCGCGCATAGCTTCCGCTGCGCTGGTGTATCGCATCCGAC
CCGCGCGCTGCTTTCATCTGGGACCCCTGCTCTGTGGCTTGGCAGGCCCAAGAAAGGCG
TGACCCGCCGCGCTGCTGCCCTCCCTGCTTGGGACCGCCCGCGGGGACGGCCGCGACCG
CAGCGGAGACAAGGACCTTCCCTGCTTGGCGGCCCTCAGCGCTGGCCCTGTGTGGGGCTGT
GTAGGAGCATGGGTCTTCGGCGAGCCCGCCAGCACTTACTGGGCCAGGCCAGTTGTCTGGC
CTTAAGTTGTACCGAAACTTACACAGCATCCACACACACACACACACACTCTCACAC
ACACTCACACGTGGAGGCGAAGGTCACACAGCATCCACTATAGTCTAGACGGCACCG
TGCTGCAGTGGGACCGGGGGGGCGCCAGACAGGCAGCTGGGAGATGGAGGACGGAGCT
GCAGACAAGGCGAGGGGACCATGCGGAGGAGGAATGCCAGACCCAGGCAGTGTGTGTG
TGAGGCATAGCCCTTGACACACACACACAGACACACACTAGGTGATGATGATGAC
ACACATCGCGCGACAGCTGCTTCCCTGAAGCGACAGTCACGACAGCATGCACAGATATG
CCGCTGGGACACAGATAAGCTGCCAAATGCACGACAGCGACAGAGATGCCAAGAAC
TACAAGGACATGCTGCTGAAGTACACACAGCACACCCATGCGCAGATGTGCTGCTGGACA
CACACACACACAGGATATGCTGTCTGGACGCACACAGTCGAGATATGGTATCCGGAACA
CACGTTGCACAGATATGCTGCTGGACACAGATAATGCTGCTTGACACACACATGCACGG
ATATTGCTTGGACACACACACACACACGCGTGCAGATATGCTGTCTGGACACGACAC
ACATGCGAGATAGCTGCTGGAACACACATTTCCAGACACAGTGCACAGGCGAGATATGCT
GCTTGGACACAGAGATATGCTGTCTAGTCACACACACAGCAGAGATGCTGTCCGGACAC
ACACAGCATGACAGATATGCTGTCCGGACACACACAGCACGACAGATATGCTGTGAC
ACACACAGATAATGCTGCTTCAACTACACACAGTCGAGATATGCTTGGGACACACAC
TGTGCACAGATATGCTGTCTGGAATGACACAGTCGAGATATGCTGTCCGGATACACAG
CACGACACAGATAGATATGCTGCTGGGACACACAGATATGCTCCGGAACACATGCACACAGGT
GCAGATATGCTGCTGGACACACACAGATATGCTGCTTCAACTACACACAGTCGACAG
TATTGCTTGGATACACACATGTGCACAGATATGCTGTGGAATGACACACACGTGCAGATA
TGCTGTCCGGATACACAGCACAGCATGACAGATATGCTGCTGGGACACACACTTCCGGA
CACACATGACACACAGGTGCAGATATGCTGCTGGACACAGCAGAGTACGTGCTTGG
GAGGCTGTCCGTGAAGCCTGCAGTACGTTGCGCTGAGGCTCATAGTTGTAGGGACTTGT
CCCTGCTCCACCTGACTCCCCAACTTCTCCCGGCTTCTGCTCCCGCTCAGTCCCGGCTCT
CATCCCCGCTGTCTCCCTGCGCTTGGCGGCTATTTTGGCACTGCTTGGGTGCGCCAG
AGTCCCTTACTGCTGTGGGCTGGGTTTGGGGGACAGAGCCCAAGCCTGAGAGCTGGAG
CCCATGGCTAGTGCTCATCCCGAGTGCACTTCCCCCTGACACAGGAAGGGGCTTGTA
TTTATATTTAAGAAATGAAGATAATATAATATGATGAAGGAAGACTGGGTTGAGGAGC
TGTGTCTCTTCTGGGGCGGGGACCGCGCTGGTCTTCAAGGAGCTGATGACACACCC
CTGAGGACACACACACCCACCCACCTGCTGTGGTGGCCCGAGATCTGTAAATTTTA
GTAGAGTTTGAAGCTGAAGCCCGGTATATTATTTATTTTATTTGTAACACAAA

MTPSPLLLLLLPLLLGAFPPAAAAAGPPKMDKVVPQRVARLGRTVRLQCFVEGDPPPLTM
WTKDGRTHSGWSRFRVLPQGLKVQVEREDAGVYVCKATNGFGSLSVNYTLVLLDDISPGK
ESLGFDDSSGGQEDPASQQWA RPRFTQPSKMRRRVIA R PVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTL SLKNLRPEDSGKYTCRVSNRAGAINATYKVVDVIQRTRSKPVL
TGTHFVNNTVDVFGTTTSFQCKVRSDVKPIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWPVIGIPAGAVFILGTL LLLWL CQAQKKPCTPAPAPLP GHRPPGTARDRSGDKDLP S
LAALSAGVGVLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHSHSHVEGKV
HOHIHYOC

FIGURE 71

CCGAGCTGAGGAGCGCCTGCTCAAAGACACGGTCACTGGATCTGAGAAACTTCCCAGGGGACCGCATTCCAGAGTCA
 AGTGACTCTGTGAAGACACCCACATCTACCTTCTGCCACGTTCCCAGGGGTTGGGGGGAAGATGTTGGGGGACCA
 AGGCCTGGGTGTTCTCTCTTCTGCTGCTGGAAAGTCACATCTGTGTTGGGGGAGACAGACATGCTCACCCAGTCA
 GTAAGAGAGAGCTCAGCGCTGGGAAGACAGACCCACCATCTCTGCAAGCTCTGGCCAGACACCTTGGAGAGCTCGG
 TGAAGTGACACATCGTTCACATCTGACTACCCAGCGGAGCGGAGCTATGAGCGCTGGACCGCATTCGCTT
 TCTACTATTGGGACCGCTGTATTGCCCGTCCCTCGGGCTAGAGGCTCGGACCACTGACTGGACACTCGGGCG
 AGCACTGGCCAGGCTGCTCATGTTAGTCCCGCTGAGGGTTTCTGGTGCTCTCAAAGGAGAGCAGCGGCTGGCCA
 GAAGCTGCTTAATTACACCGTAGCCTTCCCTCTGCCCAACAGGATCCCTGCCGCCAGACACAGCGGCATCTGGGA
 GCGCATCTGCTCCCTGGAGCAAGTGTCAAGCTGCGCTTGGTGAGACTGGGGTCCAGACCTGCGACACGCAATTTGC
 TTGGCAGAGATGTGCTGCTGCTGAGTGGCCGACGAGAGGCTGAGCACTGCAITGGCCGAGCACTGAGGCTTC
 CTCTGACTCTGACTTGGCCAAATGGCCAGGTGATGTCATCTGTTATCCCTGATGTCGAGACTCTATGCTGCTTC
 ATGGGGCTGTCTCCCTTCCCGAGGTTGCCCAGGCTCAGGGGCTGCTATCTACCTCTGACCAAGACGCGCGAAG
 CTGCTGACCCAGACAGACAGATGGGAGATTCCGAATCCCTGGGTTTGGCCCTGATGGCAAAAGCATCTCGAA
 GATCAACAAAGTCAAGTTTGGCCCCATTGTACTACAATGCCCAAGACTAGCCTGGAAGCAGCCACCATCAAGG
 CAGAGTTTGTGAGGCGAGAGCTCCATACATGGTGATGAACCTGAGACAAAGCAGGAGAGCTGGGCGAGCG
 GTGTCTCTGTGCTGTGAAGCGCAGGGAAGCCGAGCCAGACAGATTTTGGATCATATGACACATTTGCT
 GGATCTTCCCTCTACAGCACTGACAGCAGCTGCTGCTGCTGAGAACTCGAGCAGCAGCAGGCTGGGAGTTC
 TTGCAAGGCGCCAGAGTGATGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTGCACAGCATGTATGAG
 ACTCTCTTGCACCCAGGTTCTCGAGAGTATCTTATCCGGCTGCCCATGATTGCTTTCAAGATGCCACCACTC
 CTCTACTATGACGTGGGACGCTGCCCTGTAAAGACTTTGCGAGGCGAGGAGATATGGGATCAGGTGCGCGTG
 ATGCTGTGCGAAGTCTGCTGTGGCATCTCAAGACAGAGGAAAGGAGATCCAGTGCAGTGGCTACAGCTTACCC
 ACCAAGGTGGCCAGGAGCTGACGCTGCGAGGCTGACGGAACCTGGAGCATCTGTCGGCGGCGCTGTCAAGTG
 TGCTGCAATGGGAGCAATGGCTTTGCCCATGTACATGTTGGACACGCGTTGAAGCATGACTGGCTACA
 AGGGCACTTTCACCTCCATGTGCCCCAGGACACTGAGGGGCTGGTGCTACATTTGTGGACAGGCTGCAAGAG
 TTTGTCAACACCCCAAGTGTCACTTTCAACAAAGAGGGGAGTGCCGTTTCCATGAATCAAGATGCTCTCG
 TCGGAAGAGCGCCATCACTTTGGAAGCCATGGAGACCAACATCATCCCTCGGGGAGATGGTGGTGGGAAGACC
 CCATGGCTGAAGCTGGAGATTCCATCCAGGAGTTTCTACAGGCGAATGGGAGCGCTGATAGAAAGATGAG
 CCAAGTGTGACCTTCTGATCCCGGAATTTTCCACGCTCAGGCTGCCGACGATGACCTGACTTCACTCAATCA
 TGACCAAGCAGACACTTCCCTTCCGAGCTATGGCATGTTCTCTGTGAGACTCAGAGATGAGGTCACTCTCAG
 AGCCACTTAATGCTGGCAAGTGAAGGTTCCACCTTGACTCGACCCAGGTCAAGATGCGAGAGCATATCCACA
 GTGAAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAAGGTGATTCCAAATTTGAAATCCAAAG
 GAGGAACAAAGAGAGAGACAGAACTTCTCTGTTGGGCAACCTGGAGATTCTGAGAGGAGGCTCTTAAAGCTGG
 ATGTTCTCTGAAAGCAGCGGGTGTCTTGTAAAGCTGAGGGCTACCGAGTGAAGGTGTTCTGCTTATGAGCAG
 ATCCAGGGGCTGTGATCTCTGATTAACTGGAGCTTACATCTGCTTCTTCCAACTCCAGGCTGCTGCTGGG
 CCGCTTTGACATGTTCTATCAACAGGCCCAACGGGCGCTGTGTGCTCGGCTGTGATGACCAAGTCCCTGTGAT
 CCTACTCTGCTATGCTTGTGGCAAGCCTGGCTGGGAGGAAGTGAAGCAGTGGAGTCTTCTCTTAATTAAC
 CCAAATGCAATTTGGCGTCCCTCAGCCCTATCTCAACAAGCTCAACTACCGTCCGACGGACCATGAGGATCCAG
 GGTTAAAAAGACAGCTTTCAGATTAGCATGGCCAGGCAAGGCCCACTCAGCTGAGGAGAGCATTTGGGCGCA
 TCTATGCTTGTGGAACCTCCGGGATGTGAAGAGCTCATCCCCAGGCGAGCTCCGCTGAGGCCAGTGTGAACCCA
 TGGGCGATGATGATTAACAGACACTCCCTTCAACGAGAGTACCCATGAGCTGGATGAAGACTATCTT
 GGCATGGTGGCCCAAGCCGATGGAATCAGGGCTGCTATATCAAGTGAAGATTGTGGGGCGCATGGAAATGA
 ATGTGGATCCCGCAACATGGGGGCACTCATCGCGGCAAGTGGGGAAGCTGTATGGAATCCGAGATGTGAGG
 AGCACTCGGGACAGGAGCAGCCCAATGTCTCAGCTGCTGTCTGGAGTTCAGTGCAGTGGGATGCTCTATGA
 TCGAGGAGCTGTGAGCGCACCTCCGAGGTGTAAGAGCCAGCTCCGCTGAGGCCAGTGTGAACCCCA
 TGCTGATGATGACTGTGTCACACCTTGGCACTGTCAGTCAACAGCAGCAGGCTGATGATCACTGCTGGCA
 CCTCTGGACCACTTGGGCCACACATCTGCGATCTACACTGTCACTGACCAAGACCTCGCAGCCAGGAGAT
 CGCGCTCGCGCGGTGCTTTGATGGCACATCCGATGGCTCTCTCCAGATCATGAAGACAAATGGGATGAGCC
 TCACCTTCAACTGTGTAGAGAGAGGATAGGCGCGCAGAGTGCTTCCAGTACCTCCAAAGCACCCGAGGCTGAGC
 TCCCTGTCTCAGGACACTGTCCAAAGGAAGTGGCCCTCGAGGAGGCGAGCAGCGAGCAGGCGGCTGGCCAGCG
 CCAGGCTGGAGTGTGGCTCTCTGAGATTCTGTAGATTCTCAACAGCCCTGATCAACCAATTTGTGCT
 ACTTCACCTCTCTTCTGCGCATTTGATGGACACTTGTGAGACTGATGCAAACTGCTGACTTGTCTGTTAAT
 TTAAGCACTCTGTTTTCGCTGAATTTGCTGTTGTTTCTTCACTGCTTTACTTACTTTGTCCCATGCTACTGAT
 TTGGCAGTGGGCCCCACAAATGGCACAAATAAGGCCCTTTGTGAAACTGTTCTTTAAATGAACACAGAAATTT
 GGCCACTGTTAAATCTTCGACTCTCAACTGTACTTTAAATGCAATTAATGCAAAATATCTCTCTTCTTT
 TTGTCATGTTTTCGCCCACTCTGCAATAGTGATTAATCTGATGCTGAAGATCAAAATACCAATATAAGCATAT
 TTCTTGGCTCTCTCACAGGATATGCCAAGCCTGATCATGATTTCTCATATATAATGCTGTGGTGAATAAG
 AATAAACAACATATTTACTCTGAATCTAATAATATCTTATTCTTTCTTAAATTTGGAATTTCTAGTG
 ACATTTCAAAGTTAAGCTATTAAATATAGGGTGATCATAGTTCTCTACCAAGTCTGGAAGAACATCTCTGGT
 ATCCCAATTTACACAGGTTGCTTAAGTGTATTTGATGTTTCCCTTTGCAATTCGCTTTGTTGTTCTGTGAAGAC
 CCAAGTGTAGCCGAGGCGAGATGTCAAATAATGCATCTGTATTTCGAAAAA

FIGURE 72

MVGTAKWVFSFLVLEVTSLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLES PGEWTTWFNI
 DYPGGKGDYERLDAIRFYFGDRVCARPLRLEARTTDWTPAGSTGQVHVHSGPREGFWCLNREQ
 RPPGNCNRYTVRFLCPPGSLRRDTERIWSWPSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAIIYLLTK
 TPKLLTQTDSGRFRIPGLCPDGKSI LKITKVKFAPIVLTMPKTS LKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFPVPE SYLIRLPHDCFQ NATNSFY YDVGRCPV
 KTCAGQQDNGIRCDAVQNC CGISKTEEREIQCSGYTLPTKVAKES CQRC TETR SIVRGRV
 SAADNGEPMRFHGVYMGNSRVSM TGYKGTFTLHV PQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPIT LEAMETNI I PLGEVVGEDPMAELEI PSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTDLNF INDEGDTFPLR TYGMFSVD FRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRNRKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSE RFLPSEQIGGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPR
 VKKTAQFQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTVPFN
 EDDPMSWTE DYLA WPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSRRASVNPLHEYL VNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQS PAAGTVQGRVP SRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAAAGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTGGTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCCTACCTACCCGTACGCATACATACATATGTGTATATATGTAACTAGACAAAAGATCGCAGATCAATAAGC
 AAGCTCTGCTTTAGTTTCAAGAAGATTACAAGAATTTAGAGATGTTATTTGTCAGATCCCTTCGATTCATG
 CCCTTTGGGTTGCGTTTCAGTTCCTCGGATATTACCTGTGGAGACCCCTCTGAGACGTTCTGTGCAATGGGCAATC
 CAGATTTACACGGAAGAGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCAGGCACATGCAAAAAATA
 TCTGAAAGTGAACCTCGATCTCTCGGATATTACCTGTGGAGACCCCTCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCAATTAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGAGTATCCCAAGCCTCTCCAGGTTAAACAT
 CACTCTGTCTTGGAGCAAAACATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AATGATCCTGGGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGGTCTTAGAATCATTTGCACAGA
 AGAGTACTCACAGGGTATACACAAATAGCAAAATATCCACTTTGAAATCAAGACAGGTTCCGCGCTTTTGTG
 CTGGACCTCGCCTACGCAATATGGCTTCCTCTACGGACAGCTGGATACACCAAGAACTCAGAGATTCTTTT
 ACAGTCACAGACCTGAGGATAAAGCTGTTAAGACAGCCGCTTGGGGAATATTGTAGATGAGTACACTTGGC
 ACGCTACTTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCCAATGTGAGCACACACTACAGGTCCAGACTGTGGGAATGCAAGAAG
 AATATACAGGCGCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCAAAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAAACGAGCTCCTGCACTGCCAGAACCGAGGAGCGTCCACAC
 ACAACGTGCGCTGCTGTGCCCGCCGCGCATACACGGGCATCCTGCGAGAAGCTCCGGTGGCGAGGAGCTGGC
 AGCTCGGCGCTCCGACTCTGGCCAGGCGCGCCCCCGCACGGCACCCAGCGCTGTGCTGTGACCAAGCTGCT
 GGGAAACCGCGAGCCCTGTGTTCTAGGTTGTCACCTCCAGCCACACCGGACGGGCTGTGCCGTGGGGCAACA
 GACACAACCCAAACATTGCTACTAACATAGGAAACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAAGAAGGCCCTAAGTGAACATAAGCCATATTTATCACCCTGGACAGCACATCCGATCAAGATGTTAAATTC
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCACATTGCCAGCTGCAGAGCATATTGTGGA
 TTGGAAAGGCTGCGACAGCCCCCAACAGGAAAGACAAAAACAAACAACTAACCCAGCTAAAAACATTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAG
 GTGCTATTGTGGGATAAAGGAATCTGTTACAAGCTGCCATATTGGCTGCTTCCGTCCTGAATCCCTCCAAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTGGTTGAAAGATTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAACAGCCCCCTCTAAAGAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTT
 ATTTTCTTGAACCTACTGTAAATATGTAGATTTTGTGATTATTGCCAAATTTGTGTACCAGACAATCTGTTAAT
 GTATCTAATTCGAATCAGCAAGAGCTGACATTTTATTGTCCTCTTTTCGTTCTGTTTTGTTTCACTGTGCAGA
 GATTTCTCTGAAGGCAACGAAGCTGCTGGCATCAAGAATATCAGTTTACATATATAACAAGTGAATAAGA
 TCTCCACAAAGGCACTTTCAATGTTTCTGTTGCTTTAACTACGGAAGATTAAAGAATAAAAACTCCTGCA
 TAAACGATTTCAGGAATTTGATTTGCAATTTCTTAAGATGAAGGAACAGCCACCAAGCAGTTTACACTCACT
 TTTACTGATTCTGTGTGGACTGAGTACATTACGTGACGAATTTAGTTCCCAAGGAGATGATTGATGTTCACT
 AGCTTGCACACTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTAACAACGCAAAAAAATAAAAAA
 AAAAAA

MYLSRSLSIHALWVTSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLYK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYKPELQVNIITLSWSKTIETLDNIVITFESGRPDQMLEKSLDYGRTWQPPQYYATDCLDAF
HMDPKSVKDL SQHTVLEI ICTEEYSTGYTTSKI IHFEIKDRFALFAGPRLNMA SLYGQLD
TTKKLRDFFTVDLRI RLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKNYQGRPWSPGSYLP I PKGTANTCIPS ISSIGTNVCDNELLH
CQNGGTCNNVRCLCPAA YTGILCEKLRCEEAGSCGSDSGQAPPHGTPALLLLTTLGTAS
PLVG

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTT
 CTCTTGTTGGACCATGTCCGTGATCTTTTTTGCCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCGACTGGCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCCTGTGGTGGGAATTCACAGCTTCTCATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTACACACCGATGCACCTTGAGGCTGTCTCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCTCTCCCTCATTTCTAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTACCTTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTCTGCTGCTGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGCATGTCAGTGAAATCTGGGAATGGCTGGATTTCGGAACATCTGCCATGTGTATTG
 ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCATGCTTAGTACATATGACCTTTAACCCCTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTTCATGAATCATTCATATGATTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTACATGTTACACAAGCTTCTACGGTTTTT
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAACC
 TAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAATAAAAAAAAAAAAAAAAAA
 AAAAG

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKVK
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGGCGGGTGGT
 CCTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTCCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCAACACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACTTTACCCTGGCAATTGCCCTGGGTGCTGTCTCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACACTACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGGCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCTCATGCCCCTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCACTCATGCATCTCCTTCTTGGGGTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTGCTGCTGTCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGG
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGCTGACGG
 GCCTGTCTGTGCTCATTTGCGCCATCCACATCTTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCATGCAAGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCAATTAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGACACTGCCATGACGCAGATAATT
 GGGAAGTGTGTCTGTCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACACGCAGCCTTTGCAGGCCCTCACCACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCCTTGGGCTGGACAGACTGCCCTGCCCGT
 CTCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAG**TGAC**CTCCAGCTGGGGGTGGGA
 AGGAAAAAATGGCACTGCCATCTGCTGCCTAGGCCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAAGTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAAACTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGGTAGGGGCAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTGTCCTTGCGCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACTG
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVVK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIYIQLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRILLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAVIQVVLI FYLMVSSVVGFY
SSPLFRSLRPRWHD TAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTLCVLKFTTA AVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGCGGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTT
TGTCGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGCTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

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FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCA GTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCTCACTTGCAA
GGGATTTGCTTCTACTCACACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACATTATTACAAGAA
TGATAATGTCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
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FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGPFAAQANVELLGSSDLLT

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAAC**ATG**GGCTCCGAGAACCTGAGCACCTTTT
 GCCTGTTGCTGTCTATACCTCATCGGGCGGTGATTGCCGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTTAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGTTGAAGAA
 GGATTAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGAACCCCTCGTCAGCAAGACAGAAATATTTCCAAGAGGAAGTGATA
 TTATGTAGATCTAGAAGTCACTTTGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAACCGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAC TAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGG
 AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACAGGCGAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TGA**GAGTG
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCCGCTGAGT
 TTCAAGAAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAAATATAGAGGGTTGGA
 GTTGTGTAGCAATTTCAATCAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKALQLHPDRNPDDPQ
 AQEKFQDLGAAYEVLSDSEKRKQYDTYGEGLKDGHQSSHDIFSHFFGDFGFMFGGTTPRQQ
 DRNIPRGSDIIVDLEVTLEEYVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
 MTQEVVCDCEPNVKLVNEERTLEVEIEPGVRDGMETPFYFEGEPHVDGEPGDLRFRIKVVKH
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGKHVHISRDKITRPGAKLWKKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTTATCCCGACCGGAACCTGATGATCCACAAGCCCAG
GAGAAATTCCAGGATTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

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FIGURE 87

GGCACGAGGCGGGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAAGGTGTCGTGGAGGAACCTAGCACCTGCCATCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGCATGG
 AGACTGTGGTGATTGTGTCCATAGGTGTGCTGGCCACCATTCTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTGTACACTCTGAC
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCTGGACGCACGACGACTGCCCTGCTCCTGTCTGTACAG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTTAGTGCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTGTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTACATTAATAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTA CTCTCTCACCTGGCCTGTTTCATTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAACT
 ACAAAGTTGATGATTTCTTTTATCTTTATGCCTGCAATTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACCTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 89

GCTTCATTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC
CCACCAC TG CAGCC ATG ATCT CCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTTCTGTCTTTTGAATGATTCTCTTTTGTGACAAAGCACTACTGGCTAT
TGGAATATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTCAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG
GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTA TAA CAACA
AGTGAATTTGAAGACTCATTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTC
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTGTAGAAGTGCCACTGCAATGGCAAAAATATTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCAATTTTAAAGTATTAAACCAAGGAAACCCAATTTTG
ATGTATGGATTACTTTTTTTTNGCNCAGGGCC

FIGURE 90

MISLTD¹³TQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
 HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFI²⁰RRVPVLGSL²⁷LNLPGI
 RSFVDKVGESNNMV

Important features:**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

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GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGTGTCCCCACCCTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTTCTGTCTTTTGGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAAATGGTTTAGAAAGAACATTAGATCTCTCTTCCAAAACATAAAATGAAG
CTACAGTTTTTTTCTGGGTGGTATTTCAGTCTTATTGGTTGGCCTTGTATAGGCATG
ATCTCGAAATTTATGGATTTTTCTCTGTCTC

FIGURE 92

GGCAGGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCTTCTCTGAGTCTGGATCTTTCTTCTCTGGAAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGACCTCGCGGGACTGC
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTAGCTCTTCACTCTCTCTCTGGCCATTAAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTACGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCAA
TTATCGGCTGGATGTGGTACTTACCAGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTCT
GATTCATGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTCAGAAA
TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGACCTTCCCAGA
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCCTCGC
TGGTGCTCTACCCTTTCTTCCAGTTCTGTTGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGTGTCACCATCCGAAGGGAACCTTGGGGAACGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGAGGAAGATGTTTGTGAATCTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTCTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACCTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGTGAGTTTTCTGT
AACCCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

MDLAGLLKSKQFLCHLVFCYVFIIASGLIINTIQLFTLLLPINKQLFRKINCRLSYCIISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKEIDFLCGWSLSERFGLLGSGKVLAKK
ELAYVPIIGWMMWYFTEMVFCRKEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAYVDCITLNFNRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLQEKDAFQEEYYRTGTTFPETPMVPPRRPWTLLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVGRWMIGVTEIDKGSAYGNSDS
KOLGND

FIGURE 94

CTGAGGCGGCGGTAGCATGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGCGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTTCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTGTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATCCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACTTGCAGGAGCATTTTTCAAACCAAGACCTTGTCTCTGCTATTAACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTCTGAACAAGTGGGTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAACCGAAGAAATGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAATCCAAAAAGACCTCAGGAGAACATTTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCCAAATTTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
 TGTTCATAAAGTAGCTGTAACACCAACCACCTCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCTTACA
 TTTTGAATCCTTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCAAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCAAACCTTTTTTTCACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCCTTAGAATGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAATGGAAGAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAATTTTATATGAAAATTTATCTGAGTCATTAATAATCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGVEVKGAEKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRHSDQIMTFRERLHLHKNLQEH
FSNQDLVFLLLTPSIITFESCSTHRLHSLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEEELKSI CKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQDKPDQENIFLCQALRTFFPNEFLHSCVMSLKNRHSVSKS
CNYNHLDVDVNDLTMVEHTDIEPASFQNTICILKHALDLDDRWFQFKRSLRLDTQDKRSKA
NTGSSNQDASKMSSPETDEEIEKMGFGEGYSRSPTF

FIGURE 96

GGCACAGCCGCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACAGCGCAGGGCAGC
 CCAAGCAGCGCGGAGCGAAGCCCGCCGCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCCTTCCTT
 CCTTCCCCGCGTCCCCGCGCTCGCGGCGAGTCAGCTTGCCTGGGTTCCGTCGCCCGCGAAACCCCGAGGTCACCA
 GCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCCCTCCACGCCCTCCTTCTCCCTTGGCCGCGGCGCTGGCACC
 GGGAGCCGTTGCTTGACGCGAGGCGCCAGCTCTACTTTTCGCCCGCGCTCTCTCCGCTGCTCGCTCTTCCAC
 CAATCCCAATCCTTCTCCTTCCAGTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCGCGCTGCCGTAG
 CGCGCTTCCGCTCGGTTCCAAAGGTGGAAACGCGTCGCCCGCGCGCCACCAAGCAGCTGGCTTGGCTTGGC
 CGCGCTTCTGACACCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTCGACGCTCTTACGTGTCCAAAGGCTTCAACAAGACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCAGGGTCTTACTCTGCTGCTCTCAAGAGATGGAGGAGAAGTACACCTCGCAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTGGCTTACGCTTACAAGAAGTTTG
 ATGAATTTCTCAAAGAACTACTTTGAAAATGCGAGAAATCCCTGAATGATATGTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGCTCGCTCTCGAGCGGAATGTTCCGCTGGTGAACCTCCAGT
 ACCACTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAAGCCCTTCGGAGATGTCCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCGTACTTTGCTCAAGGCTTAGCGGTTGCGGG
 AGATGCTGCTGAGCAAGGTCTCGTGTTAAACCCACAGCCCGAGTGACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTGAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAAATAGTGTCAAGTGCTCAGAAGGTTTTCAGGGAGTGTGGACCCCCAAGCCCTTCCAGCTGGACGAAT
 TCTCGTCCATCTCTGAAAGTGCCTTCAGTGCTCGCTTCAGACCAATCACCCTCGAGGAACGCCAACCCACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTCCTGGTCTT
 CCTTCCGAGCAACGTTTGAACGATGAGAGGATGGCTCGAGGAACGGCAATGAGGATGACTTGTGGAATGGG
 AAAGGCCAAAGCAGGTACTGTTTGCAGTGACAGGAAATGGATTAGCCAAACAGGGCAACACCCAGAGGTCCA
 GGTTGACACCAAGCAACACAGACATACTGATCCTTCGTCAATCATGGCTTCTCGATGATGACCAGCAAGATGA
 AGAATGCATCAATGGGAACGACGTGGACTTCTTGATATCAGTGATGAAAGTAGTGGAAGAGGAAAGTGGAAAGT
 GGCTGTGAGTATCAGCAGTGCCCTTCAAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA
 GAAAGCCGACAGTCTGGTGTCCGCTCTGGGCAACAGGCTACCTCCTCACTGTCTTCTGATCTTGTTCCTGG
 TTATGCAAGAGAGTGGAGATTAATCTCAAACTCTGAGAAAAAGTGTTCTCAAAAAGTTAAAGGGCACCAGTT
 ATCACTTTTCTACCATCTTACTGACTTGTCTTTTAAATGAATGGACAACAAATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGAAGTCTGACTTGTCTTCTCATTCAGTTTGGGAGGAAAAGGAGCTGTGCAATTGAGTTGGT
 TCTCTGCTCCCCAAATCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
 TTTTATCACTCTTATTTGTTGTATGTTTCTCATTCAGTTTGGGAGGAAAAGGAGCTGTGCAATTGAGTTGGT
 CGCTTGTCTTCAACAGCAACAGGGTCCCTCTTGGCAGTAACATGTAGTATTTCTGGAATATTAATA
 GCTGTACAGAAGCAGGTTTTATTATCATGTATCTTATTAAGAAAAGGCCAAAAGC

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FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLVMQNSSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFGDVPRKLKLVTRAFAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYLEF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPQAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGAATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGC
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGTGCTCTC
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCGCTCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGC
AATCAGGAAAGTAGCAACAGAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

[illegible][illegible][illegible]

FIGURE 100

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GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGAATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
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FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGTCTTCTTAC
CTTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG
CTGCGGAACCGAGGCCAAGTTTCAGTTCTACCCACCGGGCTGCAGGGTCACTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGTCTGTCTGTGCAGAGCCCAAGGAAGTCTCTGCAGGAGTCC
GGAGAGTACTGAGACCGGGAGGTGTGTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCCTTCATGTGGCAGCAAGTTTTCGAGCCCACTGGAAACATATGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGTCTCTCCCCAGCCTCCAATTAGAACA
AGCCACCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTCGACAGTGAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTCCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAAGTGGTCAAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTAAATAAATAGACGA
AACCACG

FIGURE 103

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELF SQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHV AEPYGSWAFM
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIY LPLRGT

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FIGURE 104

GTGGGATTTATTGAGTGCAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAG**ATGT**CATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCATTTTGACCCTAAACTTTTGAAGGAA
 AAGTAAAGGAGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACCTGACGGAATGGAACGACAGAATATAACTA
 ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCCTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTACCTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAAACAGGCAAATTCACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAG**TGA**AACAGAATTTGAACGTGAAGCAAGCATTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCATATCGGTA
 GCAAGCCATGGA AAAAGATGTGTCAGCTAGGTAAGATGACAACTGCCCTGCTGGCAGTC
 AGCTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTACGCTAGCTGGTACAGA
 TAATTCAAACCTGCTGTTGGTTTTAATTTGTAACCTGTGGCCTGATCTGTAATAAAACTT
 ACATTTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINS IQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNI TNQLEKWMKLNVEEGLYSRTL AGSITTPPLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWIIPDPTGKFNLIRRYTEISNIK

TGTTTGTTCGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAAATACAGCAGACCATTNCCGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAAATTGTCAATTTTGACCTTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCCTTTCGAAGGTTCTACTTGCCAATTCCTGGTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGACAGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTGGGGCGCGGGCTGCA
 TCCGCATCTCTCCATCGCTGCAGTAAGGGCGGGCGGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTCAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTCGGGCTCAACAGTGATTTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACTTTTGAAGGTTCTACTTGCCAATTCGGGTTCCAGCGCAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCACTGGA AAAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCGCCACCTTGGTTCAGT
 GCTGGA AAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTG AAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATCCCA
 GACCAACAGGCAAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAATTTGAAGTGTAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGA AAAAGATGTGTGCTAG
 GTAAAGATGACAACTGCCTGTCTGGCAGTCAGCTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTTAATTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAA AAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCATGCGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCCTGAGAAGGCCCCACCACCCAGAAGCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCCCTCCCCTGGTCCTCCAGTGTTTGTCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCCTAAGTGGA
 T**CATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTTTTGCC
 ATGATGTTTACCTTCAGATTCATCACACCCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTGTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCCCTGCGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCT
 TTCGGGCATTGGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTCACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAGGATTCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACTGCTATTAAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCAAGAAGTCAAGTCACTTTACATCTATTAAGTGCCTTGAGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGAT**TAG**ATACCATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTTAAGAGCCATTACAGAATAGAAGATGAGACCACCTAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCCCTATTCTTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHQGTVVKGSSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

111/330
MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHQGTVVKGSSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

[illegible]

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
 PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
 SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPPIPGTTAQPVTLMQ
 LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
 RQDPGGAFFQKPGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLFLIDGSTSIGKRRFR
 IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV
 GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAEE
 NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDLACSKTCLNSADI
 GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISDTDRIGAVQYTYEQRLFEGFDKYSSKPDIL
 LNAIKRVGYWSSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
 VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAAC TGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCTTTTCCGGCTGCTCATCCGCTCGGCCCTCCTGTGCGCGCTGCTGCCTCAGCACCATTGGT
 GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCC GCCACTACAGTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGTGATTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
 TGCTCCAGGACACGCTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTCC
 TCCAGCCTTT CAGACCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAAC TACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCC TACTGGCCTGGTCTTCAGAGCCTCATGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 GTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCAACCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGC GGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTGGTTCTTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCTGGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTT CAGAAAAACACTGTTAGTTCTGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCCT
 AGACTCCTCA TAA CCACTGGATAATTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHPGPDGSAIDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPDTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS



FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGAGAGCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCATGTTTGTCTACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTGTATGTGGAGCCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCTGTACAGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTCTGAGTGTGATGTCATGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCTTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCAGTGACCTAGAAACCATGGAGCCAGGGGCTGCATCTGTGTGAAGGCCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCTTTGTGGCTTCATGCTGATCCTTGT
 GGTGCTGCCACTGTTGCTGTGAAAAATGGGCCGGCTGCTCCAGTACTCCTGTGGCCCTGG
 TGGTCTCCAGACACCTTGAAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCTGGAT
 CTCATAGGTTTTCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTACAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTTGAGTTCATTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGATGAACACGGAGGATC
 CATGAACACTACTGTAAGTGTGACAGTGTGTGCACACTGCACACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTC
 TGTTGGTAAAGTACAGAATTACGAAATAAAAGGGCCACCCTGGCCAAAGCGGTAAAAAA
 AAAAAA

FIGURE 117

MQTFTMVLEEIIWTSLFMWFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE
TVVYSVEYQGEYESLYTSHIWIPISSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS
SILKHPFNRRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPAAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVVQGEAIPVLALFAFVGFMILIV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAAACCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGTGAGTGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGC GGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCCGCACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGGCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGGCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
 TGGTAGGGGCTTGGGACCCAACCTGTGTCA GTGGAGGAGTCAAGCCCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCACAAAAATAACTTGTATCAAT
 AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAAACAATCCA
 AACAATACCTCAGATATAAAATAAAAAATGAAAGTATCCTCCTCAAAAA

120/330

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKEPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CGGACGCGTGGGCGGGCGGGACGACGAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGCGCCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGGTGTCCGCTTCTCTAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCCTCAGCTACGTTACGGGGTGACCAAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCTCTCAAGAAGTGGGCTGCAA
 GGCCCTTGTGTTCCCAAGCAATTCAAGACCCAGCAATACTACAACGCTCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTGAAGAGTCAGAGGCTCCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCCCTTTGCCGGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCTGTCTGCCATG
 ACCCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCTCTCC
 CACTACAACATTGTCAACAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTTGCCCAACCCCCGTATACCATTGCTCGGGTTCGTTGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCCTCATCCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTTCTGAACAGCCAGACTTCTCCAGTTATGACATCTCGACCCATGTGTGGAG
 GTGTCAATTGCTGGGTCCCCGTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCAAGAGAACAGTCCCGTGACATTCGCGCACTT
 CCCGTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTATGCCCTCACACGGAGG
 CCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCGTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTCCGCTGAAGGACGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCGGAAGTACATC
 GTGTTTGTCAACAACTACCCCTCACCATTTCAGGAAAGATCCAGAATTCAAACCTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCCTGTCTGGCCGGTGTGGCTT
 GACTCTCTCTGTGAGAAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGCTT
 TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACCTAAGAGCTCTCTGGATGGGTC
 CGGGAACCTCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCTG
 TCCATCCCCACATTCCCCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLSSREVD RMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLT TVISVDAPLP GTLLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLV VAYGTTENS PVTFAHFPEDTVEQKAESVG
RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGE PQKTEEAVDQDKWYWTGDVAT
MNEQGFC KIVGRSKDMIIRGENIYPAELEDFHHPKVQEVQVVGVKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKI QKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413**N-glycosylation Site:**

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTGCCAC

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FIGURE 124

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTTCGGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTACGGGC
 TTCTGGCGTTTATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTGCACCCGGCAGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCGGTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAACCCATGCCAGCGCCAACCACTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGGCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCCAAGCTGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGCTGCTACTGT
GAGCTTCTCCACCTGGAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCATTCCTGTTCCCAACCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACTTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTTCGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGCTC
 TCCGCTTGCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTGCGCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAPVRPTSTTKPMPAPTSQTTPRQGVHEASRDEEPRLTGGAAGHQDRNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAPVRPTSTTKPMPAPTSQTTPRQGVHEASRDEEPRLTGGAAGHQDRNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

[illegible]

FIGURE 128

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCTCTCTGCCCAGGGAGGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTTGAAGTGGCACGCCCTCTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
CACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAAGTCCAATAAAACATTTTCCATCCAAA

[illegible][illegible][illegible]

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATAGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTATATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATTATC
TTCATAATTAATTGTAACGATTAAGAGCAGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

131/330

FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPQTETGPKAMGDLSCGFAGHS

131/330

GGGGAATCTGTCAGTAGGTCTGCCGGCGATGGGGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGAAGTATTTATTGACCAAATTAACAGGTCCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC

TGCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCGAGAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCTATCAGATCACTAAGAACA

GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT

TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCTCTCA

GGTTCTCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC

ATGATATCATGTATCTTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT

CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTGGCCATGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG

ATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTGTTGATGCAAGATACACCAAAAAAC

CAGGGCTGGAAATCTATGAAGATACCTTAGGAAGCCAGCTGCTAAGGATGTCCATCTTGTG

GGATCACTGCAAAATACAAGTATGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA

AACACCTCTCTCTGTGGGCTACCTTGTTTTCATGTTGGTGATGAGTGGCTAGAATTCTTC

TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA

AGAGCTGTTACAATTTGTAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA

GCCAGTTTATTAGGAACCATTTCAGATGGATGACATCACCTGTTACTGGGAGAACCCTCTTG

AGTGAATACTCTAAATTCCTGTCTTATAATGTACGAGAAGGAAAGGTTATGATCAAATTTAT

TCCAAAAATGTTGAAACTGAACTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA

ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTGAATA

TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGACCCAGAGCAACTCTTGAGA

AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA

CCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAGACCAATC

ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA

TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAAATTCGTCAATTTGGAAGTAGTACAA

CTCATTGCTGGAATTGTGAAATTATTCAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG

AAACCCTATGGGGTTTATGAAAAATACTTGGGGATCATCTCTGAATGGTCTAAGGAAGCGG

TAGGCATGCCATGCAATGTAGGAGTCTCTTTTGTAAACCAATAACTCTGTACTGAC

GAGGTTTCTATAATGCCACATAGAAGAGGCCAATTGCATGAGTAATTTATGCAATTGGATT

TCAGTTCCTCTTTTGTGGCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLFLLP¹SAQGRQKESGSKWKVFIDQINRSLENYEP²CSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEV³VRRLGLGTHYQITKNRLYREND⁴CMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPK⁵WMEPAIPVFSFSKTSEYHDIMYP⁶AWTFWEGGPAVWP⁷PIYPTGLGRWDL
FREDL⁸VSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYL⁹FNFRGVAASFRFKHLFLCGSLVFHV¹⁰GDEWLEFFYPQLKPWWH
YIPVKT¹¹DLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMD¹²DITCYWENLLSEYSKFLSY
NVTRRKG¹³YDQIIPKMLKTEL

$\begin{pmatrix} 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \\ 7 \\ 8 \\ 9 \\ 10 \\ 11 \\ 12 \\ 13 \end{pmatrix}$

FIGURE 134

CACCCCTCCATTCTCGCCATGGGCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCAGGATCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
 AGGTCACTGTATGTGGCCTGCATGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGCTGTGGGTGGTGCCACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAACTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATCTTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATCTGAGTTTCAGCCA
 CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGGAAGTGTACTTGCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCACCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLLVFGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTAGAGTAGTTACAAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCACATAAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACCTTCAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGCTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAAACCATATGGC
 ATTCAGGTGGGTAAGTGGTGTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACAAAAAACCATAT
 TCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACCTGCGATGGGTTGGGTTATATAA
 TGTCACAGAGATTTGGTGCCAAAGGATCTATGAAATGATGGGTACGTAAGAACCCATCAAGTTT
 GAAGATGTTTATGTGCGGATCTGTTTGAATTTATTAAGTGAACATTATATTTCCAGAAGA
 CACAAATCTTTCTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCAAGGAGATCATCACTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAAGTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGAAAA
 GTGTTAAATAAGTAGGTACTGTGAAAAATTCATGGGAGGTGAGTGTGCTGGCTTCACTG
 AACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCTCTGTAGACTAGAATTTCTTAAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CTCTCTTACATGCAACATTTTCCAGTTACTTAAGTATCAAGTTATTTATTTATGATACATC
 TCCATTAAGTAAAGTCATAGGTCAATTATGTCATATCAGTAATCTCTTGGACCTTTGTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAGCAAGAAAACTGTAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVF IN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQ EYPFKVFPYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGCGCAGTCAGTGAGTGTCACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCCTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAGTCGATGACCTGAGCAAGTTCGGA
AAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACCGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYNGNGFAATRLFQKKTCTIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPPKGLMYSVN
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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FIGURE 140

CATTTCGAAACTAATCGTGTGAGAAATGACTTTGAAAAGCATGCTTTTTACAGAAGTATA
 TTAACCTTTTATAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTCG
 CTCATATATAGGAAAATCGCATATGGTCTAGTATTAAATTTCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTTCAGGAATTAC**ATGA**ATGACAGTCTTCGAACCAATGTGT
 TTGTTGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAACTCGTCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAGCCAAATTAAGCAAGAGGA
 TTGAATCCGGATGGAACCTCCAGCCCTTTCAACCCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTGAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTCTCTTTGAGCCTGCATCAGTTCCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTTCTTGAACCCCTCTA
 GGTCTCTAGAACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAAGAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTTTCTAAAAAAGG

FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLY
 TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
 SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
 NRRSRSGTYSRRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKSRSRSQ
 SKSRDHSDAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSGHGRHRR

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FIGURE 142

TGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTACAGAAATATAT
TANCTTTTATAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCCTTTATACCAGAAAAAGCCAAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

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FIGURE 143

GGCACGAGGCCCTCGTGCCAAGCTTGGCACGAGGGTGACCGCGTTCTCGCACGCGTCA**ATG**GC
 GGTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCAGTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTCTTGGTGCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTGACAGTGACAGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCCTCGAGCTGGGCCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAATTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCCCTCCTGC
 ACACAGCTTCTGTCTCCCTGTTTCATCCTGTGGCTCTGGACAAAGCCCATGCACGGGAC
 TTCTTGACACAGCCGCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCCTCTGTTGTCTGGTGGTGTCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCTGGGCCAGCTCCTACTATCCCCGACCCATCCTCAGCC
 AGCGTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGATTGCCGG
 GGCCCTGGGTGGCCTGCTTACTCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCTCTACTTCCACCAGCACTTGGCA
 GGCTCC**TAG**CTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GCGGTTCCCTTCACCACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACTGTCTCTCCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGAGTGGCGAGGGTGTGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTTAA

MAVLGVQLVVTLLTAPLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEEKPLSVPRDAPFQLETCLPTTVDALVLRFFLEYQWVFDAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLVYFAEEGGERSVCLTFAFLFLLLAMLVQV
VREETLELGLLEPLASMTQNLEPLLKQKGWDWALPVAKLAIRVGLAVVGSVLGAFLTFFGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLLVLLVLCLLRLACTRPHLGLGLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VSLQYLTPILITLNCITLLLTLLKQYSGWLGLGAPLLSFPDSSASAAPIGSGEDEVQQTAAIR
AGALGGLLTPFLFRGLVAYLITWTTACOLLASLFLGLYFPHOHLAS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

145/330

FIGURE 146

GGTTCTACATCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTCTCGGAGAGATGAAGG
 CGCTTCTGTTGCTGCTTTGCTTGGCTTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCTCTG
 TATTGAGAACTCTGTAAGGTTGCCCTCCACTACGGCCTGACCAAGATAGGAAGAGGGCCCTACAAGATGGCTG
 TCCAGACGGCTGTGGCGAGCCTACAGCCACGGCTCCCTCCCGAGAGGTTTCTCGACGTGCCACCATTCTCTTAA
 TGACAGACGAGCCTGGCCCTAGACAACCTGGCTACGTGCTCTCGCAGAGGACGGCGAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAATAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAATAAATCGAGCTTTGAGTGTCTTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGG
 GCAGGGAAAAATCTGAAAACACCACCTGCCCTGAAGTCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCAGTGAAGGCCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACTAGCGTGTGGCTCTCTCGGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCCGCAGCAGGAACAAATGGACAGGCCCC
 GGATGCCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACCTGGTGGCAAGGTGGATGAGCCTGGGGTTTTATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCACTGTAGGAGAAATGACCGTGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCGAGAAAG
 TGCGGCTCATCTGATTCAAGCCAGTGAAGACGTGTTCACTCTGCTGTCCCGCAGGTTCCGCGAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCATCTCAAAATTTACTTGTGATGAGAAGGTGTTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCTCGCAGGGGGAGCATCACATAGAGAATGGGATTTGCCATCTATGTGATCAGTGTGAGGCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGAATGTGGATGGGTCGAACCTGACA
 GAGGTGAGCGGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAGCTTTTGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGAATCCCAACACAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTGATGTGGCTGGAATTACACCGGTGCTGTATAACTGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGTTATGAAGAATACAATGGAACAAACCTTT
 TTTCTCAAAATCCATTGTTGAAGGAACACAGCATCAAAATGATGGAAGAATTAGATGTGGTGATATCTTCTTG
 CTGCTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGTGTCAGTGTGTTATTTAAAGAAAGAAATACATGT
 ATTAATGTGAGGAAAGTATGATCATCTAATGAAGCCAGTTACACCTCAGAAATATGATTCCAAAAAATTA
 TCAAAATAGGCTAAGAAGTTGAACACTATATTTATCTGTCAGTGTGTTATTTAAAGAAAGAAATACATGT
 AAAAATGTGAGGAAAGTATGATCATCTAATGAAGCCAGTTACACCTCAGAAATATGATTCCAAAAAATTA
 AAACTACTAGTTTTTTTTCAGTGTGGAGGATTTCTATCTACTACAACTGTTTATATTTTTTCTATTTCAAT
 AAAAGCCCTAAAACAACTAAATGATTGATTTGTATACCCCACTGAATTCAGCTGATTAAATTTAAAAATTT
 GTGATATCTGAAGTCTGCCAAGGTTACATATGCCCATTTTAAATTCAGCTTAAATATTTTTAAAAATGCA
 TTGCTGAGAAACGTTGCTTTCATCAACAGAATAAATATTTTTCAGAACTTAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
APSEVVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNMGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDPVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNNHMAPPSDWSPSWVMWLELPRCLYNCKDIVLRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHAACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTTACTTACTCCAGCACCTTCCTCTCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAAACATCATCAGCCCAGCAACAATGGTGGC
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAATAACCTG
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTTCATGTTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAAGTCAAATTAATTTCTTTCCCAATGCCCAACTAATTTTGGATTTC
AGTCAGAAAATATAAATGCTGTATTTATA

FIGURE 150

GGCACGAGCCAGGAAGTCTCACTGCCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACCTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
AGCCAGACATCGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAAGATAGGGAATGGGGAGGTGAGAGGACGCAAAGCAGCAGCCATCT**AGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCGTATTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTGCCACAAAAAAAAAAAAAAAAAAAAA

151/330

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLGVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPPIITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPILALFLYRSTRRLSEEEFG
GFRIGNGEVGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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FIGURE 152

GGTCCTTA**ATG**GCGAGAGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCCTGGGGAAGAAA
CTAAATGTCAACAACGGCCTGGAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGACC
CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCCTTTAGAGTGACAGGTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCTT
TGCCACAACATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGTACC
TGATGGAATTCCTGCACCTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTGTGTTGAAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGATTCTTTCCGTGTCCTGAAAGAG
AATTTTTAAATTATTTAATAAGAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAATAAAGAGTTCATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCQVGGQVDEKTFLL
HYDCGNKTVTPVSPGLGKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWEWDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

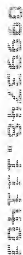
amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81



GGGAAGGCCATTTCGAAAACCCATCTATACAACTATATATTTTCATTCTGCTGCTAGCTG
CCTTGGGCTCACAATTTTCATTCTGTTTTCTGACTTCAAGTTATATACCGTGGAAATGAG
TTGATCCCAACCATAACATCGTGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTCTTTGCAGAGGATTCCACCTTCAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCAAATTGGGAGGCCAAC
CCACAGAACAGCATTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT
CCTCTCTCCAGCTCAAGCATCTCAAAGTATATTTTCAATGATTAACACTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTTACCAATGAGATAAAAAAATGCTTCTGTAT
CATCTTTTCAATAAATCTGTATTCTTTTGAATAAAAAAATAAAAAAATAAAAAA

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAAGTGTGCACCACCACACTGGAAATGCCATCCTGCTCCCGTTCTGTCTA
 CCTCAGGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGGCCCC
 AGAACTGCCCCCTCCGTTTGTCTCGTGCAGTAACCAGTTACGAAAGGTGGTGTGCACGCCCGCG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTCTGCAGT
 TGGGCAGGAACCTCCATCCCGCAGATTGAGGTGGGGGCCCTTCAACGCCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTGCACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACCTGGGCGATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTTGGTGGGGCTGGAGGAGCTGGAGATGTCAAGGAACCACT
 TCCCTGAGATCAGGCCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTAG
 AACTCACAGGTGAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACTTGGCCCAATAAACCTCTCTTCTTGGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTCCCAT
 GCACATGCGAGGCCGTACCTCGTGGAGGTGGACAGGCCCTCCTTCCAGTGTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTCCACAGTGTCTGC
 TTTACAGACTGGGGTGTACACATGTCATGGTGACCAATGTTGCAGGCAACTCCAACGCCCTCG
 GCCTACCTCAATGTGAGCAGGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCAGTCCAAGTGTATCCAGCCGCGATATACCACCTCTACCACGGTGCTCATTGAGACTACC
 CGTGTGCCCCAAGCAGGTGGCAGTACCCGCGACAGACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCCACGACGCGGAGTACAGTC
 ACAGCGCCGCCGAGCTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGCGAGTAGTGCTGCCCAATTC
 ATGACCATATTAACATAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAAACGC
 CTGGGGAACCTCTGTGACCCACAGTCACCCTATCTCTGAACCTTATATAATTAGACCCCA
 TACCAAGACAAAGGTACAGGAAACTCAAATA**TGACT**CCCCCCCCAAAAAATATATAAAT
 GCAATAGAATGCACAAGAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATATTAAGCTATGGGCTGGTTAAAAAAAACAGATTATATTTAAATTTAAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGLEFNLYLNLGMCNIKDMPNLTPLVGLEELEMMSGNHFFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLP HDLFTPLRYLVELHLHHPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LN TSNYSFFT VTVETTELSPEDTTRKYKVPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTKMQTSLDEVMTTKIIIGCFVAVTLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLP TIHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLHFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGFGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPPALPFGDLPMGYQHLHTQLQYECISFFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWPWQAIIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSFGFKNDTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMLGLVSWSYDKTCSHRLSTAFTKVLFPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCACCTTTCCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCACTAAGTACTTCTGTTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAACCTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGCCCCCTGCCTGAAGTGGGTAATATACAATGGTCTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCGAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCAATGACCCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTGAATCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGTATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAAGAGTTGTCTCT
 CGTCCAAGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGTTGCAAGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAAATA
 TGTCTATCAAATACCTCTGTAGTAAAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLIGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTTALSREQFFKVNG
FSNNYWGWWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCGCAGTTCTC
 GAGCTCCAGCTGCATTCCTCCGCGTCCGCCCCACGCTTCTCCGCTCCGGGGCCCGC**ATG**
 GCCCAGGCAGTGTGGTCGCGCCCTCGGCCGCATCTCTGGCTTGCCCTGCCCTGCCCTGGGC
 CCCGGCAGGGGTGGCCGCGCAGGCCCTGTATGAACCTCAATCTCACCCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCGCCG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCCTCCCCATCACAGAGTTCTCTGTGGGGACCTTGTGTACCCAGAACACTTCCCTACC
 CTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCTCTCCACGACCCGA
 GCAACTTCTCAAGACCGCCTTGTTTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTACCGTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCCTCGCTGAAGCTGCAGGAACCCCTTCAGGACCTCAAGTGTGGGG
 CCCACCCCTAAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGAGGAAGGGGATGGCCACC
 CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGAGCCCTGGGAGCTAC
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCTATGTGCTACACTTATCACTGTGA
 TGGTGGCCTTCATCATGTACATGACCCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACC CGGAGCCACCTCTGGGGTCAAGTGTCTGCTGCCAGATGTGCTGTGGGCCTTTCTGTCT
 GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACCCAGGGCTGTCTCCGCCCTCT
 ATAAGTCTGTCAAAACTTACACCGT**TGA**GCACTCCCCCTCCCCACCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCATT
 TGCGTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCC
 CCTCCCTCTCTGTACCCCCGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTGGGGTGTCCGTGTTGACTCCTAGGTGGGCCTGGCTGCCACTGCCATTCCT
 CTCATATTGGACATCTGCTGTCCATTGGGGTTCTCAGTTTCCCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGTCTATAAAGGGTTAAAAATCCATAACTAAAGTTGTGAT
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA
 CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTCAGATGATCAGCTCTGTA
 TCTGTTAAAGTCCGTTGGGATGCACCCCTGCACCTAGAGCTGAAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCACTTCTTGC
 GCCCTTTATAAGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACTGAGTGATTGCAGAGTGCTTTATAAATACACCTATTATTCGAAACCCATCTGTG
 AAGCTTTCACCTAGGAGAAAGGCCCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG
 TTGCTACGCGCTGTATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCAGGATCAGGA
 GATCGAGACCACCCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAAGTT
 AGCCGGGCGTGGTGGTGGTGCTGTAGTCCAGCTACTCGGAGGGCTGAGGCAGGAGAATG
 GTGCGAACCCCGGAGCGAGCTTGCAGTGACGCCAGTGGCGCCACTGCATCTCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSYLTKTVLKVSFLLHDPNFKLTALFLYSWDFGDTQ
MVTEDSVVYYNYSIIIGTFTVKLVVAEWEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFsIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCQMC CGPFLETFSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACCTGAGCTCCCAGATCT
 GGGCCGCTTGCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCACTGGCTCTGTTTTCCCA
 CAACAGACGGGACAACCTTGCAAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
 GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT
 GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
 CCCCCGTCCCCTCCCTTCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGGAATAAAA
 TGGCTGGTTCTTTGTTTTCCAA
 AA

165/330

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

0993748.11404
10411.942660

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACCATGTTCTCTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCCACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAAATGGAGCGAGGAGCCAAAGGAGAAGAACCCAGCTTTACAGCCCTACACCAC
 GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTCGTGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGGC
 GGAAGGAAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGTTAGGAGTGTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAAGAAATCATGAGTAAACATGTTCACTTAATGTGTACCGGATCTGCGTGGC
 AGCGCTGACAGCCATCATCACTACCATTGACAGGGAACAGACCAAGAAATGTTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTACAGAGAGCCATGGTGAAGGCCTG
 CCCACACGCTCTGGTTTGAAGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAAGAGACATGA
 CTGAACATGTGCAAGATAAAAAGCAAGCTGCCATTCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGAAGTTTTGAAATTTGGAGCCACAGTTTACCC
 TGTGTCTATCAAGTATGACCTCAATTTGGCGATGCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCAGATAGGGTGAAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC
 AAGGACAGGAGCGCTCCTGAGCCTGCCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCACTGCTGTGTCCTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCAGCGCCGACGCGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCCTTGTTTCTTTTACAATAAGTCTGTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGGGTTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCG
 CTCTCCAGGAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTTCAGCAAAATG
 AAGGGTTAGATTTTTATGCTGCTGCTGATGGGTTACTAAAGGAGGGGAAGGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAAGCTGTGTTCTGCTACTCCAGGCTAACCTGAACTCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTGCTCTCGGTTTCCCCTCTGTAATATGAGTCGGGGG
 GAATGGTGGTATCTCACTACAGGGCTGTGTGGGGATTAAGTGCTGCGGGTGAGTGA
 AGGACACATCAGTTTCAAGTACAGGCCACAAAACGGGACGGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAEELESWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVILASDGYIAMVGQVHGGMLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

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FIGURE 168

GCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGACCCCTGGCCCTCA
CGTCTCCTCCAGGGATGGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCAGGCTGTTCCACCATCCTGCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGACTGGGAGTTGAATCAGGCCGTGCGGACGGCGGAG
GCTCCCGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCTGGAGAGTTCAGCTCTCAGGGGTGGGGCCTGAAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTCCGGAACCCAGCCCTAGCAGCCTTCTCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPFKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTI LLAPGEFQLSGVGP

169/330

FIGURE 170

GTGGCTTCATTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGCTCTGGACCTTCAACACAACCCCTCTTGTACCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCGTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTGTGGTGCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAACTCCTAACATATGCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAATCCCCACTCAC
TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

MAGSPTCLTLIYIILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVPFDGGYSCLKSLKKNDSGIYVVGIIYSSSLQQPSTQEYVLHV
YEHLSKPKVMTGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADPDSSMVLCLLLVPLLLSLFVLGLFLW
FLKRERQEYIEEKKRVDICRETPNICPHSGENTEYDTPHTNRILKEDPANTVYSTVEIP
KKMENPHSLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCAACATGCCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAAAACCTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCAGATTCTCCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAA
ACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAACTCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAAAATCCCCACTCACTGCTCAGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACCTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAA
TTCCTTAGTTCCTAAAGTCCATACTGTAAGAGATGAAGAGTGTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGACTCCACCATCATCCCTTCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACCCCTTGACAAT
TTTTTCATGAAATTATTCCTCTTCTGTCAATAAATGATTACCTTGCACTTAA

174/330

FIGURE 174

MKMLLLCLGLTLCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKVTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

174/330
MKMLLLCLGLTLCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKVTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAAGTGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTTCATCCAGAATCCTTCAACTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAAGTAAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
TGTTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGCTGCTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAATAAAAAAAAAA

176/330

FIGURE 176

MTCCEGWTS CNGFSLLV LLLLGVVLNAIPLIVSLVEEDQFSQNPISC FEWWFPGIIGAGLMA
IPATMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNA
NCEFS LKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMA SGWRASSFHFDSEENKHRL
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FIGURE 177

GT CGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCCTCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

178/330

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGAC**ATG**GAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCT**TGA**GCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTATGAATTAAACTCG
CCCCACCACCCCTCA

180/330

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGLLAIAAGIAAVLSGKCK
YKSSQKQHSFVPEKAIPLITPGSATTC

180/330

FIGURE 181

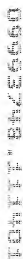
GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCC
 AGTGTTTCCACAGCCCCCAAAACGGAAGTGGTTTTGGGGTACCTGGGCGTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCCTCGGATGCTGAC
 GCCCGCCTTCCATTTCAACATCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGATAGAAAA
 GAAGCCAGCATATCTCCAGCACATGGACTTTCTGTATTACCTCTCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCAGAGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCTTAAGAGATTGAATGGGACGACCTGGCCAGCTGCCC
 TTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCAGGAAGTGCATCGGGCAGCGTTGCGCATGGCGGAGATGAAAGTGGTCTTG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGAGCCCCGTAATGTAGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAACCGTGCTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEIGILLSGGDKWSRHRRLTPAFHFNIKSYITIFNKSANIMLDKWQHILASEGS
SRLDMEFHEISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFDPAVIRERRRTLPTQGIDDFKDKAKSKTLDVIDVLLLSKDEDEG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAGAAGGAAGCCGCTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAAACCAAGAGGAAATTTGAGAAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGAAATACTGTGTTGAAGTGAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA



MYKLASCCLLFTGFLNPLLSLPLLDGREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPKKRETPDCFWKYCV

FIGURE 185

GAACATTTT TAGTTC CCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCCCTCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGAATCGCCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACTGTA

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGA
 GACAATGGAATGGAATCTATTAGGAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTTCTAACAAATGAAATATATTACAGGCAGGTACCCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTG
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCCAGCTCAGAATGAACACACCCCAACAAGA
 GCCTCCTTGTTCATAACACAGGTTACCCTACAAACCAGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCTACGGACACAGAGCTGAA
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FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGW
VVRAAHLTPLEYPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAELTPRPAGVVPGA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCGGAGCTTCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCAACCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCCTCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCCTGCCTGTGGGCTCAAATGAGCGCCTTTGCTG
 CTGTTTCCTCTGCTCCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG
 GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCACCACCTTCA
 ACACGTACACCAGGATGGTCTGGAGTTCAAGTGAAGCATAGTAAGAGCTTCAAGGAAAAC
 CCGAACTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTCGGTGCCACTGCTCTCTTTCTCTACAGCTCCATCTGTGTTTACCCAC
 CCCACATCTCACATCCAGAATCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPFCHPTLRFGGKRLMEKASLPSPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

190/330
MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPFCHPTLRFGGKRLMEKASLPSPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

FIGURE 191

AACTGGAAGGAAAGAAAGAGAGGTGAGCTTTGGCCAGATGTTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCTCTTCTTATTCTGTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCTCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCTTCCCCCTGCCCCGCCGTAGATTGAG
GACATTCGCCCCCTGTGTGCCACCAACCAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGAGCTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTCTCCCTACCCCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAGGAACTAACAAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAA

Figure 6

MWLPLGLLSLCLSPILSSPSLKQACQQLWTLPSPLVAFRANRTTYVMDVSTNQSGSME
HRNHLFCFDLYDRATSPPLKCSLL

FIGURE 193

GTAGCGCGTCTGGGCTCTCCCGGCTGCCGCTGCTGCCGCCGCCCTCGGGTCTGGAGGCCAGGAGCGACGTCA
 CCGCCATGCGCAGGCATCAAGCTTTGATTAGTTGTCTCTTTGGAGGAGCAATCGGACTGATGTTTGTGATGCTT
 GGATGTGCCCTTCCAAATATACACAAATACTGGCCCTCTTTGTTCTATTTTTTTACATCCTTTCACCTATTCC
 ATACTGCATAGCAAGAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAAGGAACCTTGCCATCTTTC
 TTACAAACGGGCATTGTGCTGTGACGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGA
 GCTTTGTGACACITGTTCTCACAGGAAACACAGCATCTCTTTGCAACTATACTAGGCTTTTTCTTGGCTTTTGGAG
 CAATGACGACITTCAGCTGCGCAGCATGGTGAAGAATACTGAACTATGTCGCAATGGACTCCCTGCTCAATT
 GTTGGCCATTTCACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCCTTGGGGGTATTTTA
 GGTGCTCCCTCTCACTTTTATTGTAAGCATACTATTTTCACAGACACTTGGTCAAGGATTAAGAAGATTCTTCT
 CTTTTGAAAAGCTTGACTGATTTCACACTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTAATGTGTTTTCTGTTAGGTGATTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCAATTTGGTTAGGAATTCAGAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTTCTTAAAAATATT
 TAGCTCCATTTATACAAAAATATAAAAATTAAGTTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACCTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAACTGTTAATGCCATGCCCTCCGTTAAGGGTTGTGGTTTTACTGGTAGACAGATGTTTGTGGATTG
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTCTCTCAATTGTTAGAAATTTATGTTAAACCTTA
 AGGTAAGGGGTGAAAAACATTTTTGAGATAAGGTTTTTATTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGGAAGAAATGACATTTGAAATCCAGTTTTTGAATCCTGTTTCTATTTAAGTGAATTTTGATCTCCATC
 AACCTTTCATGTTTTACCCTGTTAAAAATGGACATACATGGAACCACTACTGATGAGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAAAATATAGTTTAATAACACTTAGAAGTGTTTACTTACCTGGAATAATGCTATGCCGTACATT
 CAGAGTGCCCTCCCTCGCAAGGCTTGCCATGATTAAACAAGTAACTGTTAGTCTTACAGATAATTATGCA
 TTAACAGTTTAAGATTTAGACCATGGTAATAGTAGTCTTATTTCTCAAGGTTATATCATATGTAATTTAAAG
 TATTTTTAAGACAAGTTTCTGTATACCTCTGAACGTGTTTTGATTTTGAAGTTCATCATGATAGATCTGCTGTTT
 CCTTATAAAGGCACTTTGTGTGTGAGTTAATGCAAGTAGGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATCCAGTAACCCAGGCATGATCAATTTATAGTGGTCTTACATCTAATAATTATCAGGA
 CTTTTTTCAGGAGTGGGTATAAAAACATTCAAGTTGGTCTGACAGATTTTTGTTAAGGATATTTGTTGTATG
 TTTATTCAGTATACCTTACATAAAAAATTTATTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTG
 TTTATGAAGTTTATTTCTCAAGAAAAATGGGAATAAATTTGGGATTTGTTCACTTTTTTACTAAGAGTGCCTAA
 AGCCACAGGTTTTATTGGCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG
 GCGTGTGGCTGGAGCCTTCCCAGTGGAGGCTGAAAGTGGCTGTGGTATTATATGTTGAGATTTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTCTTGTGCTTGTGATCTACTGGACTTT
 TTTTTTGCAGAGATGCAATCTCTGGTCTTCCCTATTTTCTGTTCTGGATGACGTCGAGGAGCTGACTGACTG
 TTTTATCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTTTCTATATCACTAATGCAATTTGGCAGCAT
 GTGCTTGTGACCTTGATATACTAGCTTGACATAGCTGTGCTCTGATTTCTAGGCTAGTACTTGTGAGATATGAAT
 TTCCATAGAATATGCACTGATACACATTAACATCTCTCTATGGAAGAAACCTTTTGATGATGAACAATAA
 AGATTTTAAATATCTATTTTAAAAA

194/330

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLEFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

194/330
MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLEFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

FIGURE 195

CCACACGCTCGCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCC
 CACGCGTCCGCTGCACAGCTCGCGCCGACACGCTGCTGGAGGGAAGGAGCGCGGGCGGCTCTCCGCCGCTCCC
 CGCGCGCGCGTCCGACACTCCGCACCGCTC
 TCTGACGCTGCGCGGGGCGGAGCTGCTGCTTCCGCGAGTTAAAGGCTGCGCGCGCTCAGTGTGAGCGCGCTC
 CATTGCGGACATTACCGACCTTGCAGATCTGGGGAGTCCGCGCGCGGAGTTGGATTTTCCGCCAC
 AAGCTCACAGTCCGAAGCTGCAGAGGAAAGGAAGCGCGAGGAAGCGAAGCTCGGGCTCCGGACAGTGTGTTGG
 GAAACTTCCGGGCTCTAGAAAGTCCGCTCCCGCGCTTGCGCCGCGCGCTTGCAGCGCGCGAGCGAGCAGAAAGT
 GAGACATTGTCGCGCTCGAGATCGCGCGCGCGGACCGGGGCTGCTCGGAAACACAGAGGGGTCTTCTCTC
 GCCTCGCATTAATAATAGCTGCACACAAAGGGAGCAGCTGAATGGAGTTTGTCACTCTTGGAAAAGGATTTCGT
 GACCGGAGCGCTTCCAATGACACTTCCAGTCTCTCTGGAAGATTCTCGCTAATGCGATTTCCTGCTGGGCT
 CTCTGCTTACTGCTGCTCGTAGAGGCCCTCGCGGGCTGGCTTGTGTCTGCGGGGCTCTGATTCAGATGCT
 CGCGCGCGCGCGCGCGAGCTGCCCGAGCTGTGCCGCTGCGAGGGCGGCTGCTGACTCGAGGGCGCTCAAC
 TCACCGAGGCGGCCCAACCTGTCCGCGCTGCTGGGCTTGTCCCTGGCGATCTACAGAGCTCTCGGAGCTGGCG
 CGCGCGCAGTTACGGGGTTAATGCAGCTCAGCTGGCTCTATCTGGATACAATCACATCTGCTCCGTGCGAGG
 GGACGCTTTCCAGAACTGCGCGAGTTAAGGAACCTACGCTGAGTTCCAACAGCATCACCAAGCTGCCCAAC
 CCACCTTCCGCGCCATGCCAACCTGCCAGCGTGAGCTCTCGTACAGAGCTCGAGGCGCTCGCGCGCGCGAC
 CTCTCCAGCGCTGCGGAGCTCAGCAGCTCTGCGGCGCAACCATCCAGTCTGCTGCTGCGCTGCGCGCT
 CTTCAGGAGCTGCGCGAGCTCAAGTTTCTCGACATCGGATACAATCAGCTCAAGAGTCTGCGCGCGCAACTCTT
 TCGCGGCTTGTGAAGTCAACGAGCTGCACCTCGAGCACACGAGCTTGGTCAAGGTGAATCTCGCCACACTTC
 CGCGCGCTCATCTCCCTGCACTCGCTCGCTCGGGAGGAACAAGTGGCGCTTGGTTCAGCTCTCGAGCTGAGT
 GGTTTGGAACCTGGAGAAAAATGGACTTGTGGGCAACGAGATCGATACATGAGAGCCCATGCTGTGAGAGCCG
 TCGCGCACTGCACTCCCTCCAGCTGAGCTCAACCGCTTCACTACATCGAGCGCGGAGTCCCTCACTCTGAGG
 AATCCCTGCACAGCATCACTCGCGCGGAACTGTGGGATTGGGCGCACTGTGTGCGCTAGCCTGCTGTG
 GCTCAGCAACTTCCAGGGCGCTACGATGGCACTTGCAGTGGCGCGCGCGGAGTACGCACAGGGGCGAGGAGC
 TCTGAGAGCCCTGTAGCCTTCCACTGTGCGAGGATGGGGCGAGCCACAGCGGGCACTGCTCTCGCGC
 GTCAGCAACCGCAGTATCTGGGGCCCCCTGCCAGCTCGCGCGACCAAGCTCGCGGAGCGCGGGAGGGGCGAGCA
 CGAGCGCACTTCCAGCTTCCGCGCGCTGGGCTTCCAGGCGCGGAGCAGCGCGGAGAACGCGCTGAGCATCCACA
 AGGTGCTCAGCGCAGCTGGCGCTCATCTTCTCTCATGCGGGCTGTGTGCTCTAGCTGCTGCGAG
 TTTTCCAGCGCGCTCAGCAGCTCAGCAGCTGCTTGTACGCGCGGAGGACCAAAAGCAGAACAGAC
 CATGATCAGATGCTGCTCATGTCTGCCAGGAATACTACGTTGATTACAAACCGAACCACTTGGAGGAGGCC
 TGGTGTATCATCAAGCAGTATGCTCGTGTACCTGCCACAGCAGCGCGCGGAGGAATGCGAGGTGTGATTCTCC
 CAGTGGCTTCAAGCCATGGCTCCGCAAAATACGCTGGGCGAGCGGGAGCGCGCGCGCGCGCGCGCGCTGGGT
 CTCTTGTCTGTGCTCTGATATGCTCTTGTACTGAACTTTAAAGGGATCTCTCCAGAGACTTGACATTTTATG
 CTTTATTGTGCTTAAACAAAGCGAATTAACACCAACAAACCCACCCACACTCTCAGCAGCTC
 TATCTTAATTTATATGAGAACTCTTCTCTCTTGAAGATCTGTCATATCAGGAATCTGAGATGTAAA
 AAAGTGGCCATAGACAGAGAGAAATAATCGTCTTGTTTTATGCTACTCTCCACACTCGCCATGATTAA
 AACATCATGTATGTAGAAAGATCTTAAGTCCATACGCATTTCATGAAGAACCATTGGAAGAGGAATCTGCAATC
 TGGGAGCTTAAGAGCAAAATGATGACCATAGAAAGACTATGTTCTTACTTTGTGTGTGTGTCTGTATGTTTCTGGG
 TGTGTGCTTCTTAGGCAAGCAAGCTTGTCTACAAAGCGGAATTTAGTCTACATCATTTGACGCGCGCT
 GCTCTAGCTCTGAGAGTGTGGGGGAGCTGGGGGAACCGAGATAGGGAAGCTGATTTTATCT
 AAGCTTTTGTAACTTTGAATCTTTTCTTCTCAAATTAATATCTTTAGCTTCAAGAAACTTGTCTCGACCC
 CACTTAAGCAAACTACTAAGCATTTAAAGAGAATCAATTTTAAAGGTGTAGCACTTTTATTTATCTCTC
 CCACAGAGGGTGCTAATCTCATTATGCTGTGCTATCTGAAAGAACTTAAGGCGCAACTTCAAGCTCTCGTCTG
 GGCATTGTGATGATTGACCCCTCATTTGCAGTACCTTCCAGCTGATTAAAGTTCCAGCAGTGGTATTGAGTT
 TTTGCGAATTTATATGAAATAAGCTCTTTCCAGTACGAAATGACACTCTACAGAGTTTATGCGCTAGTA
 GTTTTCTAGGTTGACCGAGGAGCAGGTTAATGAGCTCTCTCTGCTGCTCATCAGAAAAAATAGGCAT
 CCTGATGCTCAGATCTTAGCTCTGATATTAATAGTTGAGACCACCTACCAACATGCAAGCTATCTCCAGAG
 ACTTCAAAAGTTACCATCGAAAGGAAGGTTATCCAGTAAAGGAATAGTTTCTCAACCATTTAAAAAATAT
 TCTTGAGACTCATCAAGATGAGAGGCGCCCAACTTTTCTCTGCGCTTCAAGAAAGGACAGCATTTGTAAG
 ATTTAGCATCAACACACATTTATGAGTATTTGATGATTAATCAGAGGGCAATGGCACTTGTATTTATCCCA
 AGTTTTCAGGACAGTACACATCTCTGCTAGGTTTGGGGCCACTTGTCTTCCGCTTTATTTATTTAGTCA
 CTTGTCAGCAAGTTTGAAGCTAGTCTTCTGACATGGCCGACAGAGGAGGATGATGAGTACATGAGAT
 GGTAGAAGGAACATCATCATTAACCCCTCTCACAGAGAAAATTTATCAAGAGGACGAAATTTATCTGTTTGG
 AGCAAGAGTGCATATAGTTCCAGGGTAGTCAAAATAAACATAAATTTCTCTCTAGATGATGGCGGATGTG
 GCTGATTGGGTCTGCCATTGACAGATGTCAAAATAAAAGGAATTAGCTAGAATATGACCATTAATGTGCTT
 CTGAATATATTGAGATAGTTTGAATGTCA

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCFQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRI FQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVICALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAETSG
HLLSAVTNRSDLGPPASSATTADGGEGQHDGT FEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQAAMSAQEYYVDYKPNH
IEGALVIINEYGSC TCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTTCGACAGCAA
CTGGAGCCAGAACCAGACCCCGTGCGCCGGCGGCCCGTTGAGTTCCCGGCCGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGA
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGACGATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGCGCGCTGACGCTG
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLPLDGLVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFVGLGPGASFVRVRSISALGRFTTRDEDLAVFLASR
AGRLRFHGFGLSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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[illegible]

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGGTTCTCCAGTCAACCTCCCGCGGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGCAACTACCATCCATAGCCCAATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAATGACTTCGAAATTTATCTTGGTGTCCTTCATACCTTGTCTGCACTGAGTCTTTC
 AACCCACTTTTCTCTCCAACTAGACCAGAAAAGGTTCTACTAGTTTCTTTTGGATGGATTCCGTTGGGATTACT
 TATATAAAGTTCCACAGCCCCATTTTCATTATATTTAGAAATATGGTGTTCACGTTGAAGCAAGTTACTAATGTT
 TTTTATACAAAACCTACCTTACCACTTATACTTTGGTAACGGCCTCTTGCAGAGAAATCATGGGATGTTTGC
 AATGATATGTTTATCTCTATTCGGAACAATCTTCTCTCTGGATCAGATGAATATTTATGATTCACAGTTT
 GGGAAAGAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTTCTACTCATACATGCCTTACAATGAGTCAGTTTCATTGGAAGATAG
 AGTGTCCAAAATTTGTTGAATGGTTTACGTCAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTG
 ATGACATGGGCCACCATTTGGGAGCTGACAGTCCGCTCATGGGGCTGTCTATTCAGATATTGACAAGAAAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAAAGTTGTGAACACTCTGAACCTAATCATCACAAAGTATCATGG
 AATGACGCGAGTGCTCTGAGGAAAGGTTAATAGAAGTTGACCACTACCTGGATAAAGACCACTATACCTCGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAAATTTGATGAAGTCTATGAAGCACTAATCTACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGAGCTTCCAGAAAGGTGGCATTACAAATACACAGTCGAATTCA
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACCATTTCACAGAATAAGTCAGATGACTTTCTGTTAGGCAAC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCATGGTCTCTGCCTTCAGAAAAGATTTTC
 TCAAAGAAAGCCATGAATCCACAGATTTGTACCCACTATATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATCTTGGAAATGTCAGGATCTGCTCAATTGAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCCTGGTAGTGTTAAACAGCAGAATATGACCAAGAGGGGTATACCCCTTATTTTCATAGGGGTG
 TCTCTTGGCAGCATTATAGTGATTGTTATTTTGTAAATTTTCATTAAAGCATTAAATTCACAGTCAAAATACCTGC
 CTTACAGATATGCATGCTGAAATAGTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGGATTTCGATA
 TTGAAGTGGAGATTCATAATATATGTCAGTGTTTAAAGGTTTCAAATTTCTGGGAACAGTTCCAAACATCTGC
 AGAAACCATTAAGCAGTTTACATATTTAGGTATACACACACACACACACATACACACACACGACCAAA
 ATACTTACACCTGCAAGGAATAAAGATGTGAGAGTATGTCCTATTTGCTAGCTAGCATAGGGATAGATAAG
 ATCTGCTTTATTTGGACTTGGCGCAGATAATGTATATTTTAGCACTTTGCACTATGAAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCTCTGATGGGTACTTTAAATTTGAATGCACTTTATGGACAGTTATGCTCTATAAC
 TTGATTGAAATGACAACCTTTTGACCCATGTACAGAAATCTTGTACGCATTTGTTCAAATGAAGGAAATTT
 TCTAATAATCCGGAATAATGAACATAGAAATCTATCTCCATAAATGAGAGAGAAGAAGGTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGACCTTGAATTTGGAGATGTATCCCAACAGCAGAAATGCAACTGTGGGCAT
 TTCTTGCTTATTTCTTTCCAGAGAAGTGGTTTTCATTATTTTCCCTCAAAGAGAGTCAAATACAGAG
 ATTCGTTCTAAATATATTTCTGTCATATAAATTTATGATTTTCCGTAGAGTATATTTACTGTGATTTTCA
 TAATAATGAAGACACATGAATATACCTTTCTCTATATAGTTACGAATGGCTGAGATAGAGAGCAACGACA
 CCATCTCAGCAATGTTTCTCTGTTTGAATTTATTTGCTCTTTGAAATTAATACCTATTAATACATTAA
 AATCAAATGGATAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
ITNQ RAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGyliQMLKKAKLWNTLNLIIITSDHGMTQCSEER
LIELDQYLDKDHYTIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-
372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCCACGGGCGGGACCTTTGTAAGTGCAGGGAGGCCAG
 GACAGGCCACCCCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCTTGCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAAGTACAA
 CCAGATCCAGAGGCAACAGGGAC**ATG**GCCACCTGGGACGAAAAGGCAGTCACCCGAGGGCC
 AAGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCTGGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCCTGAGTTCTTTACCCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTTCATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTGAC**TGAT**GAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCCTGACAGTCACTGGCCAGTTA
 TCATTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCAAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMMSKFLRHFTVVGGDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSHRFQVIIICLVVLDALLVLAELIDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

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[illegible]

FIGURE 206

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKLK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIFMAYEQIKRLVGSQDETLEIRLHVAGSLAGAIQSSIYPMEVLKTRMAL
RKTGGYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTGAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCACAGTGCTCTGGGCATCCCAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCCGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTTGGCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAATCTTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTGATGTGAAGTAGACAAGTGTGTTAAGAGTGATAAG
 TAAATGACGCTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTATGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTTCCA
 CAAATTAAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAA
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FIGURE 208

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

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FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMFFL
LNQCGSLLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPIPLPFPLQLFCFLVAIRVFPFPWTVVRKTEAGVWD

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FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTCATTTGTAAAGCCAGTGCTGCCAAGGAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCCTCCCCTGAAGAAGCTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG
 AATCTAATGGAACCTTCCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT
 CAACGTCAGTAACGCCACCTGTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCACGCTGTCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCTCTTACCTCTTGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTTGAGGTCTGGGGCTGCACCTTTGCCAGCACCCATTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
 AAGCACTGGTTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

[illegible]

FIGURE 212

MKGILVAGITAVLVAAVESLSVCVQCSWEKSCVNSIASECPSHANTSCISSASSSLETVPVR
 LYQNMFCSAENCSEETHITAFTHVHSAEEHFHVFSQCCQGECSNTSDALDPPLKNVSSNAE
 CPACYESNGTSCRGPWKCYEEEQCVFLVAELKNDIESKSLVLKGCNSVNSNATCQFLSGENK
 TLGGVIFRKFECAVNSLTPTSPATTSNVGSKASLYLLALASLLLRGLLP

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCCA
GGGCTTGCCCTACTGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCCG
GCGCGCTGCTGTGGGTCCTGCTGCTGAATCTGGGTCCCCGGGCGGCGGGGCCCAAGGCCTG
ACCCAGACTCCGACCAGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG
CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACTGGGTCTACCCCGAGCCGGTGGCCGTACCCCTCACCCACAG
CCATGCCATCTCCTGAGGATCTGCGGGTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGACGGAGCACAAGCCTTGCACCTATCAACAATGTC
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCTCTCAGAGCACCACCACTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
GACAGAAACAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAAACCTGGAAAA
CACAA

FIGURE 214

MVPAAGALLWVLLLNLPRAAGAQLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMPWGPPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQPCPNRLREECPLDTSLCDTNCASQSTTSTRTTTTTFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNLSVVFTEMQPIDRNQR

FIGURE 215

CCCGGGTGACCCACGCGTCCGGGGAGAAAGGATGCGCGGCCTGGCGGCGGGTTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGGCGGCTCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAAGTGCAGAGACA
 GAACTGCTCTGGGGGCGCTCTGAATCACTTCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 CTGCGGACGACTTAAGTATAGTGTATGTGGGTCAACGTTGGGCTCTACCTCCAGGAAGTTCACAAATGGCT
 CAGTTCATGGCAAGTGGCCCTTCCCGGTTCTGTCTTTCAAGAGCCGGCATCGGCCGTGGCCCTCGTTCT
 CAATGGCTGCCACGCTGGTGTATGCTCTGCGGTACCGACCTTCGTGCCAGGCTCTCTCCCCATGTACCA
 CACTGTGGCTTCGCTGGCTTCGCTCAATGCATGGTTCTGGTCCACAGTCTCCACACCAAGGCACACTGAC
 CTCACAGAGAAATGCACTACTTCTGTGCTCCACTGTCTACTCTACCTCAATCTACCTGTGTGCTGGTCAAGAC
 CGTGGGGCTGCAGCACCCAGCTGTGGTCACTGCCTTCCGGGCTCTCTGCTGCTCATGCTGACCGTGACGCTCT
 CTAACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCTGTGGCTGTGGAAACAGCGCGCGCTGCTCACGTGCGCAAGTGGTGGTGGTGGTCTT
 GCTGCTGACGGGGCTGCTCTGCTCGAGCTGCTTGACTTCCACCGCTCTCTGGGTCTGGATGCCCATGCCA
 TCTGGCAGATCAGCACCATCCCTGCCACGCTCTCTTTTCAGCTTTCTGGAAGATGACAGCCTGTACTGCTG
 AAGGAATCAGAGGACAAGTCAAGCTGGACTGAGAGACCTGGAGCGAGTCTGCCCGAGTGGGGATCTGCCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTCAACTTCTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTGGAGTCTGTTCTAGGG
 AAGGCTCCCAGCATCTGGGACTCGAGAGTGGGAGCGCCCTTACCTCCTGGAGCTGAACTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGAGGACAGCTGCTGTTTCTCTCCACAGCCTCTCTCCACATCCCCAGCTG
 CTTGCTGGTGGTCTTGAAGCCCTCTGTCTACCTGGGAGACAGGAGCCACAGGCTTAGGGATACAGGGGGTCCC
 CTCTGTTTACCACCCCCACCTCTCCAGGACCACTAGGTGGTGTGCTGGATGCTTCTTTGGCCAGCCAA
 GGTTCACGGCGATTCTCCCATGGGATCTTGAGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCACTCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCCCTCACCATACTCCCTTTAGGGCCAGGCTCCAGCAAGCCAGGGCA
 AGGATCCTGTGCTGCTGTCTGGTTGAGAGCCTGCCACCGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGG
 TGACAGGGCGGTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGCGCAGTGTGGAGACGGGTGTTGT
 CGGGGAGAGGTGTGGCTCAAAAGTGTGTGTGCGAGGGGGTGGTGTGTAGCGTGGGTAGGGGAACGTGTG
 TGGCGTGCTGTGGCATGTGAGATGAGTGACTGCCGGTGAATGTGCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCCTGTCAACCATCAATATCACTGTGGAGCCCACTCTGCCAAGACGCCACTGGGCGGACAGC
 CAGGAGCTCTCATGGCCAGGCTGCTGTGTGCATGTTCCCTGTCTGGTGGCCCTTTGCCCGCTCCTGCAAA
 CTCACAGGGTCCCCACACACAGTGCCCTCCAGAAGCAGCCCTCGGAGGAGAGGAAGGAAATGGGGATGGC
 TGGGGCTCTCTCCATCTCTCTTTTCTCCTTGCCCTTGCATGGCTGGCCTTCCCTCCAAAACTCCATCCGCT
 GCTGCCACCCCTTGGCCATAGCTGATTTTGGGAGGAGGAGGGGCGATTTGAGGGAGAAGGGGAGAAGCT
 TATGGCTGGGTCTGGTTTCTCCCTTCCAGAGGCTCTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCC
 ACATATGCTGTGCTCTGGTAAAGGTGACCCCTGCCATTACAGCAGGCTGGCATGTTCTGCCCCACAGG
 AATAGATGGAGGAGCTCCAGAACTTTCCATCCCAAAGGAGTCTCCGTGGTTGAAGCAGCTGGATTTTG
 CTCTGCCCTGACCCCTTGCTCCTCTTGGAGGAGGGAGCTATGCTAGGACTCCAACTCAGGGACTCGGGTG
 GCCTGCGTACTCTTTTGATCTGAAAACCTTTAAGGTGGGAGGTGGCAAGGATGTGCTTAATAATCAA
 TTCCAGGCTCAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTGVLQYQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAWFSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFESFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

GGCCGCGCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCTGTA
CTATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
CTGATGGCCGCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC
CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAAGAAACCAAGCCGAGGAGGAGC
TGGATGCCGAAGTCTTGAGGTGTTCCACCCGAGCGATGAGTGGCAGGCCCTTCAGCCAGGG
CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGGCAAA
ACTCCAATATGAGGACAAGTTCGCAAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA
ACACCTACACATCTCAGGATCTCAAGAGTGCACCTGGCAAAATTCAGGAGGGGGCAGAGATG
GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA
GGAACCTGAAGAAAGACTTTGATGAGCTGAATGTTGTCTATTGAGACTGACATGCAGATCATGG
TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTCTTGGAAAGAGAGATTGCTGCGCTG
TTTGATCTTGAATATTATTGCTTCATCAGTAGGACATGCGCAGAGACCTGCTTTCCCTTTGGTG
TCTTCAAGTGGTGATCAATGGGCTGAACACGACAGAGCCCTCGTGAAGGAGTATGCTGCGT
TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA
GCCCTGCAGAAGCTGCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAGAAGAGGTT
CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCTCTGAAGC
TCGGGGGGCTGCAGGTCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
CGCGTGTTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCGCCAGGAGGAGGCTGA
GCTGACCCAGGAGATGTCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
GCCTGTGGGAACAGGGCTGTTGCGAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGAT
GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGCTACCG
TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
AGCTTGCTGAAGGAGCTGAGATTGAGGCCCCACACCAGGACTGGACTGGGATGCCGTAGTGA
GGCTGAGGGGTGCACSGCTGGGTGGGCTTCTCAGGCAGGAGACATCTTGCCAGTCTGGCT
TGGCCATTAATAATGGAACCTGAAGGCCAAATTAACAAAAAAGAAAAAAGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPKESSSTKETTERKETKAEHEEL
 DAEVLEVFHPHTEWQALQPGQAVPAGSHVRLNLQGTGEREAKLYEDKFRNNLKGGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHMDNAQDLLSFGGLQVVINGLNLNSTEPLVKEYAAAF
 VLGAAFSSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVRLTLVQEKGEVLAVRVVTLTYDLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCCCCTCCC
 CTCCCCCGGGTCTGGGGGTGACATTGCACGCGCCCCCTCGTGGGGTCGGGTTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCGCTGTCTGGTCAGGCCCCACCCCC
 TTCCCACTGACCAAGCA**A**TGGGGGCTGCGGTGTTTTTCGGGTGCACTTTGTCGGGTTCGGC
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTGGT
 CGCAGGGGCATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTGTGTGGTCTGGTTCATGTTGG
 TCCATGTGACCGACCGGTGAGATGCCGGCTCCAGTACGGGCTCCTGATTTTTGGTGCTGCT
 GTCTCTGTCTTCTACAGAGGGTGTTCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCGGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTGGCT
 GATGCATTTGGGCCAGGTGTGGTGGGATCCATGGAGACTCACCTATTACTTCTGACTTC
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTTGGTGGTGGGAGTCACCTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTACGGCGAGCC
 TCTGTGTAAAGACT**G**ACTACCTGGACTGATCGCCTGACAGATCCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTCTGTCTCCTTCTCGTC
 GGCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTTACGCCAGTCAGTACTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTCACTGCTCTGCTCTCAC
 CTTGCCCAAGACTCACCTCCCTTCCCTCTGCGAGCCGACGGCAGGAGGACAGTCGGGTGAT
 GGTGATTTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG
 GTTGCCAAAGAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAAACCTAAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTCAACCTCCTTGGGCTATATTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTCTCCTTGGTCCCAGACCTT
 GGGGGAAGGAAGGAAGTGATCTTTGGGAACTGGCATTACTGGAACATAATGGTTTTAACTC
 CTTTAAACACCAAGCATCCCTCCTCTCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTTGTAGTTTTTAATGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGT
 ATCATTTTCTGCTGAGGGTGGAGTGTCCTATCCTTTTAATCAAGGTGATTTGTGATTTGACT
 AATAAAAAAGAATTTGTAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MGAAVFFGCTFVAFGPPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLASVWVILVHVTDR
SDARLQYGLLIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIGHDSPYYFLTSAFLTAAIILLTFHWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFNLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

GACCGACCGTTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTNTCTGTTATCAATATTTTGGNGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTTCGGCCCGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCTCTGTGGTCTGGTTCATCTGGTCCATGTGAC
CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

GTAAAGAAAGTGGCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTCCCTTCCCGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCATTGCTGTCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGCTGCGGTGTTTTTCGGGCTGCACTTCGTCGCGTTCGGGCCGCGCTTC
GCGTTTTCTTGATCACTGTGGCTGGGACCCGCTTCGCGTTATCATCTGGTCGAGGGG
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGTCAGATGCCCGGCTCCAGTACGGCTCCTGATTTTGGTGTCTGTCTCTGTCT
CTTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGTGTGAGGACGGAAGATCAACCATCTCCATCCGCCAGATGGCCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTCTCTCTTCAATATTTGGCTGATGCACTT
GGGCGAGGTGTGGTGGGATCCATGGAGAC

FIGURE 225

GCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTGTGACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGTGTCT
 AGACTCCTATCTTCTGAATCTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTGTGGTTCCTCTCTACCTGGGGAATAAGGTGCAGCGGCCATGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCAACAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCTGGCCACTCT
 AACGACCTCATGCTCATCAACTGAACAGAAGAATTCGTCCCACTAAAGATGTGAGCCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGACAA
 CCAAGAGCCCCAAGTGCATTCCCTAAGGTCCCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGAGATTACCCTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTATTCTCTCCAGAGATGTTGAGAATGTTTATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTGTGCTTCCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCGAAATAAA
 CTGAGAAGTGGAAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSI PHPGYSHPGHSNDLMLIKLNRIRPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGD SGGP
VVCNGSLQGLVSWGDYPCARP NRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGCGGGCGTGCCTCAACTTGAGGACCGGGCCGCGCA
 CAAGCCGAGCGGGCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGCGCCCTGGCTGTGCT
 TGCTGGCTGTAGCTGTCAACGGTGCCGTGCTCTTCTGAACACGCCCAGCGCGGGGACG
 GCGCCCCACCTGTGCTGACACTGGGGCTGCCAGCGCCAAAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACGCTGCACCTCAGCATPCTCATTGACCGCGCTGCCCGGACCTCACCGACA
 GCTTTCGACGCTGGAGAGCGCCAGGCGCTCGGTGCTGCAGGCGCTGACAGAGACCAAGGCG
 CAGCCACGGCTGGTGGGCGACAGGAGCAGGAGTGTGTGGACACGCTGGCCGACCACTGCC
 CCGGCTGCTGGCCCGAGCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG
 GCACGCTGGGCGAGGCGCTCAGCGCCCTGCAGAGTGAGCAGGGCGCGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCGTCAGCGACATCTTGGATGCCCT
 GCAGAGGGACCGGGGGCTGGGCGGCGCCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC
 GGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGGCGCCGAGACTGTCTGGACGTCTCT
 CTAAGCGGACAGCAGGACGATGGCGTCTACTGTCTTCCACCCACTACCCGGCGGCTT
 CCAGGTGTACTGTGACATGCGCACGGACGGCGGGGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTTCTTCGGGGCTGGGACGCTACCGAGACGGCTTTGGCAGGCTCAC
 GGGGAGCACTGGTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCACAGGCT
 GCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCGCTATGCCCGCTACGGGAGCTTCGGC
 TGGGCTTGTCTCCGTGGACCTTGAGGAAGACGGGTACCCGCTCACCCTGGCTGACTATTCC
 GGCACTGACGGCAGTCCCTCCTGAAGCACAGCGGCATGAGGTTCCACCAAGGACCGTGA
 CAGCAGCACTCAGAGAACAACCTGTGCCGCTCTACCGCGGTGCCCTGGTGGTACCGCACT
 GCCACAGCTCAACCTCAATGGGCGAGTACCTGCGGGTGCGGACGGCTCCTATGCCGACGG
 GTGGAGTGGTCTCTGGAACGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCGGCTCGGGAGGAGCC**TAG**ACTGGTGACCTTGTCTTGGCCCTGCTGGTCCCTCTGCG
 CCCATCCCCGACCCCACTTCACTCTTCTGTAATGTTCTCCACCCACCTTGCCCTGGCGGAC
 CCATCTCCAGTAGGGCGGGCGGCCATCCCTGACACGAACTCCCTGGCCGGTGGTGAAGT
 CACACATCGCCTTCTCGCGCTCCCCACCCCTCATTGGCAGCTCACTGATCTCTTGCCCT
 TGCTGATGGGGCTGGCAAACTTGACGACCCCACTCTGCTGGCCCACTGTGACTCCGG
 TGCTGTTTGGCGTCCCTGGCCAGGATGGTGGAGTCTGCCCCAGGCACTCTGCCCTGCCG
 GGCCAAATACCGGCATTATGGGGACAGAGAGCAGGGGCGACAGACACCCCTGGAGTCTC
 CTAGCAGATCGTGGGGAATGTCAAGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCTCCAG
 CCTCCCAATGCCAACCCCAACCCGTTTCCCTGGTGCCAGAGAACCCACCTTCCCCCAA
 GGGCCTCAGCTGGTGTGGGCTGGGTGGCCCCATCTTACCAGGCCCTGAGGTGAGGATGGG
 GAGCTGCTGCCCTTTGGGACCCACGCTCCAAGGCTGAGACCACTTCCCTGGAGGCCAACCCAC
 CTGTGCCCCGGCAGGCTGGGGTCTGCAGTCTCTTACCTGCTGTGCGCCACCTGCTCTCTG
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGTCCCCGGCGTCTCTCACTGGAGGGGCG
 CGGGGCTGCCATCCATTCTCTGCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGACTGCTCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCTAGGCAGGGCTGGGATGAG
 GCTTGTACAACCCCAACCAATTTCCAGGGACTCCAGGGCTCCTGAGGCGCTCCAGGAGG
 GCTTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCTTGGC
 ATTGACGCTGGCCACTGACCCAGGCGAGGCCCGGCCCGGCGAGTGGTCAAGGGACAGGGA
 CCACCTCACCGGCAAAATGGGCTCGGGGGGACTGGGCGACAGACAGGCAACCTGGACA
 CTTTCTGTGTAATCTCCCAACCCAGCACGCTGCATCCCCACTCTTGTGTGCACACA
 TGACAGGTGAGACCCGAGGCTCCAGGACCCAGCACGACCAAGGCGAGGCTGGAGCCGGG
 TCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCTGCGCTTACGTGAGGCCAGATGACAGG
 CGGCTTTTCCAAGGGCTCCTGATGGGGGCTCCGAAAGGGCTGGAGTCAGCCTTGGGGAGCT
 GCCTAGCAGGCTCTCTCGGGCAGGAGGGGAGGTGGCTTCTTCCAAGGACACCCGATGGCA
 GGTGCCTAGGGGTGGGGTTCCGTCTCTCTCCCTCCCACTGAAGTTTGTGCTTGAACA
 AACAATAAATTTGACTTGGCACCACCTGGGGGTGGTGGGAGAGGCGGTGTGACCTGGCTCTC
 TGTCCTAGTGCCACAGGTCATCCACATGGGCGAG

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FIGURE 228

MVNDRWKTMGGAAQLEDRPRDKPQRPCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDAQEQELLDTLADQLPRLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAARYGSGFVGLFSVDPEEDGYPLTVADYS
GTAGDSLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

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FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTGAACTAGCTCAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACAGGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGTGTGAC
 TTTGTGCTTGGTGCTGTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGTGCAGCCCTTGTACAG
 AACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAATAATTTCTGCCTTAGTGAAACTCTACCATGCTGAGAGATAAACAAACAAGAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTACCAGCCCAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAAATGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTATGCAGTATTAAACAGTCACA
 AGAAGTCTTATTATCATGCCACCAACCACTCAGAAACCCATAATGTCTCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCCTTACACTTGGTGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCCAGATTGTACC
 AGCAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCATCTGCCTTGTCCATGCGGTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAAATCTCAATGCCTTATAAGCATTCCTTCTGTGCCATTAAAGACTCTGATAATTG
 TCTCCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCCTTCTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTCTTCCATTGACCCATATTTATACCTTTTACG
 GTACTGAAGATTTAATAATAATAATGTAATACTGTGAAAA

FIGURE 230

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSRPRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGNTGCAGCAT
GTGGCTGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

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FIGURE 232

GCGGAGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTCGGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCGGGG
 CCCGAGCCCTCCGAGTCCGCCCTCCCGGTCGCCGCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTTCGCGGGGCGGGGACCCGCGTCCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTCGGGCCCGCAGGGGCGCTGGCCGTGGGCATCTCCTGGGCTTACCCTGAGCTG
 GCTCAGCGTCACTTGGGTGGAGGAGCCGTGCGGCCACGGCCCGCCCACTTGGAGACTCTG
 AGCTCGCGCGCGCGGCAACACCAACGCGGCGCGCCGCCAACCTCGGTGACGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGCCGGCAGGCGCGGGGAGAATTGGGAGCCGCGCTTTCGCC
 CTACCACTTGCACAGCCCGGCCAGGCGGCCAAAAAGGCGCTCAGGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGTTGGCGGTGCTGACCTCTCAGACCCAGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGCGACCGGCTGGAGCGTGTGGTGTCTGAC
 GGGCGCAGGGGCGCGCGGCCCACTGGCATGGCAGTGGTGACCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTCTTCTCTGGTGCCTGACACCACTACACCGAGGCGCACGGCTGGCACGCTTAACCTGG
 CCACCTCAGCCTGGCCTCCGCGGCCACCTGTACCTGGGCGGCCACGAGACTTCATCGGGG
 GAGAGCCCACTCCCGGCGCTACTGCCACGAGGCTTTGGGGTGTGCTGTGCGCATGCTGTG
 TCTGCAACAACCTGAGCCCACTTGGAGGCTGCCGCAACGACATCGTCAGTGGCGGCTTGA
 CGAGTGGCTGGTTCGCTGCATTTCTGATGCCACGCGGGTGGGCTGCACTGGTGACACGAGG
 GGGTGCACTATGACCTATGTCAGCTGAGCCCTGGGAGCCAGTGAGAGGGGACCTCAT
 TTCCGAAGTGCCTGACAGCCCACTGTGCGTGACCTGTGCACATGTACAGCTGCACAA
 AGCTTTGCGCCGAGCTGAACCTGGAACGACGTTACAGGAGTTACAGTGAGGAG
 TCCAGAATACCGACCATCTGGCCGTTGATGGGACCGGCGAGCTGCTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGAGGAC
 GCACGCTTTCTCTGCGCCGATGGCTACCCCGCTGCCACTGCGTGGGCTGACCGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACACCCCGGCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCGGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCGCAGGAGGCGCGCGGCCCTCACTC
 GCGGAGTGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCCCTCAGTCTCACTGTGCTGCTGCCCTTAGCTGCGGCTGAGCGTGACCTGGCCCTGG
 CTTCTTGGAGGCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCGCAGCGCTGGCCATGCAGATGTCTTCGACCT
 GTCAAGGCCACGTTGGCAGAGCTGGAGCGCGCTTCCCGGCTGCCCGGCTGCCATGGCTCAG
 TGTGCAGACGCGCACCTTCACTGCGCCTCATGATCTACTTCCAAGAAGCACCCGCG
 TGGACAGCACTGTTCTGCTGGCCGGGCCAGACAGGCTGCTCAGCGCTGACTTCTGAACCGC
 TGCCGATGCTATGCTATCTCCGCTGGCAGGCTTCTTCCCATGATTTCCAAGCCTTCCA
 CCGAGGTGTGGCCCCACCAACAAGGGCTGGGCCCCAGAGCTGGGCGGTGACATCTGGCCGT
 TTGATCGCCAGCAGCGCAGGCGCTGCTTCTACAACCTCCGACTGCTGGCAGCCCGCTGGG
 CGCCTGGGCGGCGAGCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACAGCT
 GTTCTTCCACTTCTCCAGTCTGCATGTGCTGCGGCGGCTGAGGAGCTGACCGGCTGCGCT
 ACCGGGCCAGACGTCGAGCGCGAGGCTCAGTGAGGACCTGTACCACCGCTGCCTCCAGAGC
 GTGCTTGAGGGCTTCGGCTCCCGAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGG
 CAACAGCACT**G**ACCCACCTGTCCCCGTGGGCGGTGGCATGGCCACACCCACCCCACT
 CTCCTCCCAACACAGAGCCACTTGCAGCCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCC
 AAGCTGCGCCACTGTGTCCTCTCTGGCTCTGTGGGTCCCTGGGCTCTGCACAAGCACTGG
 GGAGCTGCCCCAGAGCCACCTCTCTATCCAAACCGAGTTTCCCTGCCCTCGAGCTG
 GCTGATTGGGCTGTGGCCTCCAGTATTTATGAGTACAGCTGCTGAGCGAGCCCTGC
 CTCGTGGGCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGAGCTGAGGAGGGG
 GCATCTCCCACTTCTCCCTTTTGGACCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGAAAAA

FIGURE 233

MRASLLLSVLRPAGFVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQLLVAVL
TSQTTLP TLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLLLE
QHGDDEFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDWLGRCIL DATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALT AHPVRDPVHMYQLHKAFARAE LERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPFVGI PAPS RPASRF EVLRWDFTEQHAFSCADGSPRCPLRGADRADVADVLGTAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTL DLQLEALTPQGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAF FPMHFQAFHPGVAPPQGP GPPELGRDTGRFRDQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLR AVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTGGAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTC**ATGG**CGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCAGCGAGGGCTCCCGGCCGCCCGCGTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCAGGACGAAAACCTGTATGAGAAGAACCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTGTGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGCTCTGAA

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCGCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACCTTGATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTCTGCTCGTGGGCGCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTCATACCCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGACCTGTCACTTACACAAGGCTTTTGGAGGACCGGATCTAGTGGGGCCACCCTTCTCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAACCTCACC
 CCTTGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACCAGCTACCACTCCCAAGGAGTGCATATCCGCCCCGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAAGTTGTATTTGATGCCTTC
 ATCAGCGGGCAGGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCTCAGCGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACACGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGAGCTCATCTTAGGCAT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACTCTCGAAACCT
 CAACATCCAGCTCAAGTGGGAAGAGACCCCCAGAGAATGAGGCCCCCCAGTGCCTTCTCTGC
 ATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACAGCCTGCCAGGACCGGCTGCAACCCCACTTCTTGAGATGCTGATTGAGCTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAAGCGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTCGCCA
 GCATGGTAGCAGCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCAGGAGCCCCGACAGGT
 GGCTTGGCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACT**TGA**TT
 CTTGCCCTTTCCAGAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCTCAGAGTTGGCTTTTGAACCAAAGTGCCTGGACCAAGGTCAAGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGTAATTGAATTAA
 CTTAGAAATTCATTTCTCACTGTAGTGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGATTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGCTGTACACAGTGTATGTCACTGTGTAGTGGGA
 TGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCARNARCTSSISWELRQTLSVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWPYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVS IQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPTDFSMYPNVICLTCTVVAVCYGSFYNLLTRTFHIEEPTGGLA
KRLANLIRRARGVPPL

CAACATCGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCACAGTGACACGTACGC
TGCTTCAAGTCCGATCTCTCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACGTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGGAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCTGAGCCAGGATGGGAGGCCAAGTGTCAGGC
TCCCTCTCTACCAGGTGTCTTCAAGAAATGATGTCTGGGTCTTCTACCTCTGGGGGTCACTC
TCACCTTGGCACCTGCCCCTGAGGGTCTGAGACTTGGAATATGGAAGAAGCAATACCCAAAC
CCACCAAAGAAAACCTGAGCTTGAAGTCTTTTCCCCAAAAGAGGGAAGAGTACAAAAAG
TCCAGACCCAGGGACGGTACTTCCCTCTCTACCTGGTGCTCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAACAGTGCCCTTATAAGAGACCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCAGACCTAGAAGGCATGTGAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGTGTGCTTGTATCTTGGACTTCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMSLVLTVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEKGKDEEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

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FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACCTTCTTGGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACTTCC
 TCTAGAACCCGAGCCACCACC**ATG**AGGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAGG
 CGTCCAGTGGTCTTGCTTCTGGCTGTCTGGTCTTCTTCTTCCGCTTGGCCTCTTTTA
 TTAAGGAGCCTCAACAAAGCCTTCAGGCATCAACGCACAGAGAACATTAAGAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGCAACCATCTA
 TGCAGAGCCAGCGCCAGAGAAACATGCCCTCAACACACAAACCCAGGCCAAGGCCACACCA
 CGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAGAGAAAACCATGGTGAACACATGTCT
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGCCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTGAGAGAAGCACAGGGCCAAAGCGGCAACCACAGCCAAGACGCTCATTCCTCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAG
 AGCCCCACGACGACAGAGAAACCAAGACTGAAGCGCGCCAACTTCAAACTGAGCCTCGGTG
 GGATTTTGAAGAAAAATACAGCTTCGAAATAGGAGGCCCTCAGACGACTTGCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTGCCTGTGGCTCCAGAACTCTTTCTGCCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTTGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGAGAAAGTCTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGATCACTCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTCAGAACAGGATGTGGGGACTC
 GGACATCCTTACCGCTTTACCGCCTTCTCCCTGACCCAGTCACCTCTATATTTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGCTCCGCTACTTGCACCTTCTTGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGGTGATGTCAAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTTGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCCTGGGGCCCTCCTGTGCTCACTGGCCTTC
 AGCTCTGTGACCAAGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGATAATCCGGCTGTACCAGCGTCTCTGGTC
 CCGGAACCTGCCAAAGCCAAAGAACT**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGGCTCAGACTAA
 GCTCCAAGCCCTTCAAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTTCTGAAGTCTCTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTAAATTAAATGGGGTGATGGGTGGCCCAATACCACAATTCTGCTGAAAAACACTCTT
 CCAGTCCAAAGCTTCTTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAATCTCACTAC
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGCTCTATACCTTGTCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTGTAGAAAACATGATAATAACAAATGATTGTT
 GTCCATGGAAGGCCAAATAAATTTTTCACAGTGAAAAA

FIGURE 242

MRSCLWRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHRQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDGRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWSQDTKTTQGNGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGAVSTRTRQKGVTTAVIPPEKEKQATPPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPPFGFMEELNYSLVQKVVTFRPPVPQQQLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFL
 RYMKNRFLRSKTLDGAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGGACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCCTTGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTTCAGACAGACTCTTCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTATCTGTCACTTATTT

Figure 6

MRGPGHPLLLGLLLVGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKH FHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

FIGURE 245

GGGCTGGGCCCGCCGCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCTTCTCTGGGAGG
 CCCGACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTCT
 GGTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCTCTGTTCCGTGTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACCTAGA
 ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTCACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTGACAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRGSHWPGFNCEFFTFCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVPYPQDFKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGCGCGCAAGGGTGAGGGCGGCCCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAG**AT**GGTGTCTTCTGCCCTCAAATGGTCCCTTGCAACCATG
 TCATTTCTACTTTCTCTACTTTGGCTCTCTTAACTGTGCCACTGCCATGATGGTGTCAGAG
 CTAGGAAGCATCTCCAAACGTAAGTGATGGGACACCATTTCTTGGAAATAAAATACCACTTC
 CTAGTAGCGTCACTCCAGTTCTATTGATCTCTTGATCCATGAAACCTTACCAGCGTGACC
 TTCTGGGGGACCCAGGAAGTAGAAATCACAGCCAGTCAGCCACACAGCACCATCTCTGCA
 TAGTCACCACTGCAGATATCTAGGGCCACCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG
 AAGAACCCTTCGAGGTCTTGGAAACCCCCCTCAGGAGCAAAATGCATGTCTGGCTCCCGAG
 CCCCTCCTTGTGGGCTCCCGTACACAGTTGTCTTCACTATGCTGGCAATCTTTCGGAGAC
 TTTCCACGGATTTTACAAAGCACCTACAGAACCAGGAAGGGGAAGCTGAGGATACGTAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAAATTAAGAAGAGAGCCAGGACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA
 AGATGAGCACCTATCTGTTGGCCTTCATCATTTAGATTTTGAGTCTGTGACGAAGATAACC
 AAGAGTGGATCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGGCGTGACTCTTCTAGAAATTTTATGAGGATTTTTCAGCATACCGTATCCCC
 TACCCAAACAAGATCTTGCTGCTATTCCCGACTTTCAGTCTGTGCTATGGAACCTGGGGA
 CTGACAAACATATAGAGATCTGCTCTGTTGTTGATGACAGAAAGCTCTTCTGCATCAAGTAA
 GCTTTGGCATCACAGTCACTGTGGCCATGAACCTGGCCACCACTGGTTTGGGAACCTGGTCA
 CTATGAATGGTGAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG
 TCTGTAGTGTGACCCATGCCTGAACCTGAAAGTTGGAGATTGTTTCTTTGGCAATGTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCTGTGTACACCTGTGGAATAATCCTG
 CTAGATGCCGGAGATGTTTGATGATGTTTCTTATGATAAGGAGCTGTGATTTCTGAATATG
 CTAAGGGAGTATCTTAGCGCTGACGCAATTTAAAGTGGTATGTGACAGTATCTCCAGAAGCA
 TAGCTATAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGATTGTTGCCCTACAG
 ATGGTGTAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATTCATCTTCATCCTCACAT
 TGGCTCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGGACATTTGGACATTCATCACC
 TCCCTTAATAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGGCTCTGACGGGCGCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCACC
 AGCAAAATCCAACATGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCCC
 AGAAGAGGTGGAATGGATCAAAATTTAATGTGGGCATGAATGGCTATTACATTTGCAATTACG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACACAGAGCTCAGCAGT
 AATGATCGGGCAAGTCTCATTAAACATGCATTTAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAGGGCCTTGGAATTTATCCCTGTACTGAAACATGAAACTGAAATATGCCCCGTGTTTC
 AAGTTTGAATGAGTGAATCTATGTATAAGTTAATGGAGAAAAGAGATGATGAATGAAGTG
 GAAACTCAATTCAAGGCCTTCTCATCAGGCTGCTAAGGGACCTCATTTGATAAGCACAGATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACACTACTCTCTCGCCTGTG
 TGCACAACTATCAGCCGTGCGTACAGAGGGCAGGAAGGCTATTTTCAGAAAGTGGGAAGGAATCC
 AATGGAAACTTGAGCCTGCCTGTGCGAGTGACCTTGGCAGTGTTTGCTGTGGGGGGCCAGAG
 CACAGAAAGCTGGGATTTTCTTTATAGTAAATCATGTTTCTTTGTCAGTACTGAGAAAA
 GCCAAATTTGAATTTGCCCTCTGCAGAACCCAAATAAGGAAAGGCTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAAACTCAGGAGTTTCCACAAATCTTCACTCACTTGG
 CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAGGAAAAAAGCTGGAACAACTTG
 TACAAAAGTTTGAACCTTGCTCATCTTCCATAGGCCACATGGTAATGGGTACAAACAATCAA
 TTCTCCACAAGAACACGCGCTGAAGAGGATTAAGGACTTTGACGCTCTTTGAAAGAAAAATGG
 TTCTCAGCTCCGTTGTGTCCAACAGACAAATGAAACCATTTGAAGAAAAACATCGTTGGATGG
 ATAGAATTTTGTATAAAATCAGAGTGTGGCTGCAAGTGAAGAGCTTTGAACGATGT**TA**AAAA
 TTCTCCCTTGGCCGGTTCCTGTTATCTCTAATCACCAACATTTTGTGAGTGATTTTTTCAA
 ACTAGACATGGCTGTTTTGGCTCCAACCTGGAGATCTTTTTTCCCTTCACTCATTTTTTGA
 CTATCCCTGTGAAAGATAGCTGTTAGTTTTCATGAATGGGCTTTTTCATGAATGGGTTTGA
 TCCTACCATGTGTTTTGTTTCTACACAGGTGTGCCCTGCAACCTGAAACCAAGTGTGGGT
 TCCTCGCCACAGAATAAAGTACCTTATCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

00003740.1.1.40.1

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPWCQSTEASPKRSDGTFPPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFTWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE
 HPPQEQIALLAPEPLLVLGPLYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPCFDEPAFKASFISIKIRREPRHLAISNMFLVKSVTVAEGLIEDHFDVTVMKSTYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLFEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVRFLKTKTDVLI LPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKRDNMNEVETQFKAFLIRLLRDLIDKQWTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC
 RTQNKEKLQWLLDESFGDKIKTQEFFQILTIGRNPVGYP LAWQFLRKNWNKLVQKFELGS
 SSIAHVMVGGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTETIETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGCAGCGCTGCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTTGGGCCCTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTTCATCGGGGGACCACCATTTATGACACACGGAAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTTCCAGAAGACCACCATCCACTCAGCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTC
 CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGGCCACTCATTGTTATGATGGGTACATTTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTACAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGTAACCACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGGCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTACCCTGCTGTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTT
 CCATTCTGTCCATGAATCATCTTCCCCACACAATCATTATATCTACTCACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGGAAGTGGCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCCTTTCA

FIGURE 250

MSAVLLLALLGFIPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
 ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
 PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPPQPGCN
 LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
 LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSSVLLN
 SLFPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCFRGATHCYDGYIHLGGGLSTKMSIQGC
 VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC
 PSC

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FIGURE 251

GCGACGGGCAGGACGCCCGCTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT
 CAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGCTCAT
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCCAGCTGTCTGCGCAGGGCCGCGGGGCGACGCTGAGCATGCCAAGGACGAGGTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAA
 GAGAACATGTAGCCTCAGGCTGGGGCTGCCATTGGGGGCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAAGTGTTCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCA
 ATGTGATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAAGTAGTTAAGTCCAAAAA

FIGURE 252

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E P G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

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FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTCTAGCCAGTTCCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**ATC**AGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTT**ATAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTTACCCCTTTCTCTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCCTGGTGTGGAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTCTATTCCTCAACAATAAAGGATTTTTCATATGAA
AAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATITGAGCTGTCTGCTCGCTGTGCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCTGTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCCTGGTGTTGTCATCCCCTTGGGGC
 TGCTGTTCTCGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACCTCTTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCGAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG
 CTGGCTCAGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
 TTGAGACAGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCT**TAG**ACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTGAACTCCTAGGCTCAAGCAATCCTCCTGCCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTCCCTGTGCAGAGCCTGCCTCGTTGCCCTCATGTCACTCTTGTTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGACCCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCTTCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGAAAACCTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCCAGCTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAA

256/330

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATGGG**
GTCTGGGCTGCCCTTGTCTCTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCTCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGAC**AGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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FIGURE 259

AATTGTATCTGTGAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAAGCTCTTTAAACAATTAACTGTTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTTCAGTGTTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCCCTCCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGTCCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGATTTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTGTGAATAGCCTTTGAAATTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECVLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

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GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
GAGAGAGGCCACGATAGAAGAGTCCCTGCTTGGTGTGTTGCGAGGATGATGGTGGCCCTG
CCGAGAGCTTCTGCATTGCTGGTTGCTGCTTTCGAGCTTTTCGCGCCCGCCGAGTGATC
CCGAGGCCACCGATGGTGCAATTACATCTACACCGCGCTTTCGAGTCTTGGAGACAGGGCTGG
AAAAATTGACCAAGCAACGAGGCGATACATTCAAGAATTCAAAGATTCCTAAAAATATGA
TCTGTCATGCTGGGAAGATCTACAGACTACACAAGTAGTACAAGTGCAGTGGGTAACTT
GGCAGTGAGATGTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTC
ACGAGTGCATCGTATACAGGACAAGACATGGCAAAATGTTGCTCCAAAGAAGTGAAGAA
GAGAAAAGATCCGCGATCTGCTGAATCGAAGCTGTGACACATGCTGATGGGCATAAAGTCT
TTGAAAATAGTGAAGAAGATGATGACACATCGGCTTGTGGATGAAGAAGTGTGCTGTATA
ACTCTCCAAAGGCTGTACTTATTAATTGATTCGAGAACCAACAGCTTTGGGAATTGTGCAAC
ATACGGCCATTTCATGGAGTAAACCAACGACGCTCCCGGAAGCAAACTCTAACACTTTC
CTGGCGGGAACGCGCAAGTGTCTACAAAGTTTTCATGTTTTTCATAAACCCAGCAACT
CTAATGAGATAATCAAAATAAACCTGCAGAAAGGAGCTTGTGAAGATCGAATGCTGCTCCA
GGAGGGGTAGCCGAGCATTGTGTTACAGCACTCCCCCTCAACTTACATTGACCTGGCTGTG
GGATGAGCATGGGCTCTGGGCCATCACTCTGGGCCAGGCCATAGCCATTTGGTCTCA
CAAGAATTGAGCGGGGACATCGGAGTGAGACATTACGGATACCCCATCGAGAAGCCAG
GATGCTGAAGCGCTATTCCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCA
GGGGCTCATGCGATCCGATCTATGATTCACCTGGGCATTCAGTGAGGAGAGATTCG
CCAACTTGTTCTTCCCAAGAGCCAAAGATGCTCATCATGATCCATTACAACCCAGAGA
AGCAGGCTTATGCTCGAATGAAGAAACGAGATCTTTACAACCTCCAGACAAGAGAA
GCTGCCTCTGAAGTAAAGTCATTACAGCTGTGAGAAAGAGCACTTGGGCTTTGGCAGCTGTT
TACAGGACGTTGAGGCTATAGCCCTTCACAATATAGTATCCCTCTAAATCACACAAGGAAG
AGTGCTGTAAGATGGAAATACGTTATGCTCTTCTCCAAAGTGTCACTGCTTGGTATCTTTC
CAGAGCTTATGATGAGCATATCATCAGGAAAGTTTCAACAAGTGTCCATTACTCGTCCAAA
CCTGCTGGCTCTCAGGATGACCAATCTGTATACGCGTACTCAAGGCTTTGTTTTACT
GCTCCCCAGCATTTACTGTAACTCTGCCATTCTCCCTCCCACAATAGAGTTGTATGCCAC
CCCTAATATTACCACCTGGCTTTTCTCTCCCTGGGCTTTGCTGAAGCTCTTCCCTCTTTC
CAAAATGCTATTGATATCTCCCAATTTTCACTGGCCCACTAAAAATACTATTAATATTTCTT
CTTTCTTTTCTTTTTTTGGAGACAAGGTCTCATATGTGTCGCGAGGCTGGTCTCAAACTCC
AGAGCTCAAGAGATCCCTCGCTCAGCGTCTCAATAGTACCTGGGATACAGGATGTGCCAC
CACACTGGCTTAAAAATCATATTCTTATTAGGTTTAACTCTTATTTCCCTACGCCCTGTC
CTTCCATCAAGCTTGGTAGATGTAATTAAGAGAAATATTAACATTTGAATATCGCTTT
CCAGGTTGGAGTGTGACATCATGAAATCTCGTTTCACTTTGTGAAACATGCACAGT
TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAATTAACAAGTGAAGATACAGC
TAGAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT
TGTTCACTCACTCTATAGTACATCGGCTCATGCTTTACGCCATAAAATTAAGTGTCTGCC
TTAGGACGATTTTCACTGCTGCACAGACGCTTTCGATAGGCCCTTCAAATGATATTCCTCC
AGAAAACCAAGCTCAAGGGTGAGGACCCCACTCTAGCCCTGCTTGTCTTGTCTGCTGCTCTGT
TTCTCTCTTCTGCTTTTAAATCAATAAAGTGACATGCTGCAGAAAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAESEEKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPFRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 263

GGGCGCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAACATGGAGCTCTCGCAGA
 GTGCGGAGCTCATGGGGTGTGCGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGGC
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGCGCCCTGCCAAAAAGC
 AAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACATATCAGCGGATTC
 GGAAGGAGAAGCCTCAACAACACAACCTTACCCACCGCCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCTGCGAGCAGAGCACCAGCAGCA
 TGAGAGCCAAAGCTGGAGCTGGACCACGCCACCCTGGTGCGCTTACGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAAACGGGGACACCTCCGTGCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTACAGCCACCCAGAGGACTTCCCTAAAAAGCACAGGCGCCTGTCTA
 TCGACATTTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTCT
 CTCACTCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACAGATGAACAAAC
 ACACGCTGCTGATCTCCCTGTGGCAGATTGTAGCCTCGTGTGGCTTACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAGAAGGGGAGTTCCAGGAGTGGTGCGAGCCTTCGAA
 CTAAGGGCCACTCCGCGGCTGTGCACTCGTTTGCTTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCAAGGATGGTACATGGAACCTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGTGTAAGACAGGCCGCTTTGAAGAGCGCGGGTGCCGCGCCGTGCCCG
 CTGGCCCTCTCCCCAACGCCAGGCTTTGGCCTTGGCCAGTGGCAGTAGTATTTCATCTCTA
 CAATACCCGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCA
 ACTTGTCTCTTTGACATCACTGGCCGCTTTCTGGCCCTGTGGGGACCCGGCGGTGCGGGCTG
 TTTCAACAACCTCTCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCAAGAGACCTGA
 AGAGCCTGGGTGCCCTGAAGAAGTCACTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCCTCCTCATGGCACTGCTGCCATCTTTCTCCAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTCCATTGAACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTGTGCTGTGACTCCTCCTGACTAGTGGCCAAGGTGCTTTTCTCT
 CTCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGGAG
 AGGAGAGAGAGAGAATGTGATTTTGGCCCTGTGGCAGCACATCTCACACCCAAAGAAG
 TTTGTAATGTTCAGAACAACTAGAGAACCTGAGTACTAAGCAGCAGTTTTCAGAGGA
 TGGGAGACTGGGATAGCTTCCCATCAGAACTGTGTTCCATCAAAAGACACTAAGGGATT
 TCCTTCTGGCCCTCAGTTCTATTGTAAAGTGGAGAATAATCCTCTCTGTGAACCTCTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAT
 AGTACTATTGTCCAATGTATGAAAGTGGTAAAGTGGGAACCAAGTGTGCTTTGAAACCAAA
 TTAGAAACACATTCTTGGGAAGGCAAGTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTGGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCACTTCTCAAG
 TTCATCAGATATTGAGTGGCCACTCTGTGCCCAATAATATGAGCTGGGGATTAAAAAA
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FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWLSLKGQVLSTINTNQMNNTHAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLLKRASNESTRQLRQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCTAGTAACGTGTGTCTGACTGTGTGATCACAGGGGCGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGACCCCGCT
 GGGGCGGGAAGGCAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCTCCCCAGGTGACCTGCTCTCTTCTCGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTCGCCTGACCCCTCAGGCCCTTACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCAGTCAGCCTGTGGCTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCTATGCCCTCAGAGGCCCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

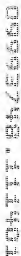


FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGCTTTTC
 CTTCCAGGACCCAAGTTTCTTCCCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTATCCGTCTGGGAGTGTGGTACAACTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCCTCAGAGAAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGTATT
 GTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCTAAGGCCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

MSFLQDPSFMTMGWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSLMDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKFKYGPQRRKMMFMGFIRLGVVYNFFRAWNGGFSGNLEGEFILGGVFV
VSGSKQGILHEHREKEFGDKNLLSVLEAAKMIKPQTLASEKK

ACGGAACCGAGGGTTCGAGGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG
GGCCAGGTGCCCGCTGCGAGGTGCCCTGGCCGGAGATCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCTCGGCGCTGCCAACCCGCCACCCAGCCATGGCGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGCCCTGCCGTTCTGCTGCGCCGCTGGGGCCGAGCTGGGGGCAAATACA
GACCACTTCTGCAAAATGAGATAGCACTGTTTTGCCTTCATCCACCACTCCAGCTCCGATG
GCAACCTCGGTCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCTTGGCTGTGGGGCTGGCACTGTTGGTTCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCATGCAGCCGAGGCCCGGGCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCATGCCCATTAGGTCCCTCTCTCTGCATCTGTCTTC
CTTCAATGTCTGTGACCTTGGGGAAGGAGCTGCCCTCTCTGGGCACTCAGATCCACCCAG
TGCTTATATGACGAGGAAGAAGGTACTTCAAGAGCTTGCCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTCAAACACAGCAGAAATGACATTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAATAAAAGAAAAGTGTTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAATGTTGCCAAGGAAAAAAAAA

272/330

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 274

MGLFRGFVFLVLLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRFFFKNVSIILPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLKGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCQGGGCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAQKHFLLOTVENGSWVGMVHFDSTATIVNKLIIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLT DGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMKNKDVSFSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSLKVRAGH
 GANTARLKLRPPLNRAAYIPGWVNGEIEANPPREIDEDTQTTLEDFSRTASGAFFVVSQV
 PSLPLPDQYPPSQITDL DATVHEDKII LTWTAPGDNFDVGKVQRYIIRISASILDRLDSFDD
 ALQVNTDLSPKESKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSANIAQVTLFIP
 QANPDDIDPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCG
 GGCAGGGGTGACAAAGGTGTATCTTTTGTATCTCGTGTGTGGCTGCCCTTCTTATTTCAAGGAAGAG
 AGCCAAAGTAAATTTTGAACCCAGAGGAGCAATGATGTAGCCACCTCTTAACTTTCCCTTCTTGAACC
 CCCAGTTATGCCAGGATTTACTTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTCGGGCTTAACTT
 GTGGTTTGAGGAGAGAACCCTTTGTGGGGCTGCGTTCTCTTAGCAGTGTCTCAGAAGTGACTTGCCTGA
 GGGTGGACAGCAAGAAAGAAAGGTGCCCTCTTGCTGTGTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGGTGAAACCTTTGGAGATTTCACTTCAGTCATTTGCTTTGCGCTGCAGAGATCTCTTTAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTAACTCCAGAGGCGAGACTCTCTAGAGAAGAAATGGATGG
 CAAGCAGCTCCGGGGGCGCAACGCATGCTTCTCTGTCTGCTGAGCCAGGGAAGCCCTTCGTGTGGG
 GCCCCGGCTTTGAGGGATGCCACCGCTTCTGGACGATGGCTGAATCTCTGAATGATGATGGCTGGCG
 GGGGGCTGCTTGGCTGGATTTCTCCGGGTGGTGGTTTGTCTGGTGTCTCTGCTGTGCTATCTCTGT
 CTGTACATGTTGGCTGCACCCAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCCAACAG
 CCCACGGGGAAGGAGGGGTACCAAGCCGCTCTTCAAGAGTGGGAGGAGCAGCACCCGCACTACGTGA
 GCAGCTGAAGCGGCAAGTGCACAGCTCAAGGAGGAGCTGCAGGAGAGGATGAGCAGCTACAGGAA
 TGGGCAGTACCAAGCCAGCGATGTCTGTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAAACCCAG
 GCGCAGCTCTTGGCCCTTCTGCACTCGCAGGTGGACAAGGCAAGGTTGAATGCTGGCGTCAAGCTGG
 CCACAGAGATTGACAGCAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG
 CCTTACCCGCCACCCCGAGGAGAAAGCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCATT
 GAATCAGCCTTGGAGACCTGCAACATCTCGAGAGAACAGCCCCAATCCACCGTCCCTTACACGCGCT
 CTGATTTCTAGAGAGGATCTACCGAACAGAAAGGACAAGGGACATGTATGAGCTCACCTTCAA
 AAGGGTACCAACAAACGAATTTCAAACGGCTCATCTTATTTTCAGACATTTCAGCCGCTCAAGGAAG
 AGAAATGAAAGCTCAAGATGGCCCAACACGCTTATTAATGCTTATCTGAGCTCAAGGAAGGTTG
 ACAAGTTTCGGGAGTTCTGCAAGATTTCAAGGAGATGTGCTATTGAGCAGATGGGAGAGTCCATCT
 CACTGTGCTTGGTGAACAGCAAAATTAAGTAACTTACGAGCAGATGGGAGATGGGAGAGTCCATCT
 CTGCGCAACTTTCGAGAACTTTACCTTCACTCAGCTGAATGGAGAACTTCTCGGGGAACAGGATCTG
 ATGTTGGAGCCGCTCTTGAAGGGGAAGCAAGCTCCTCTCTTTTCTGTGATGTGGACATCTACTT
 CAGATCTGAATTCCTCAATCAGCTGTAGGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGT
 CTTTTTCAGTCAGTACAATCCTGGCATATATACGGCCACCATTGATGCAAGTCCCTCCCTTGGAAACAGC
 AGCTGGTCATAAAGAAGGAAAGTGGATTTTGGAGAGACTTTGGATTTGGGATGACCTGTCAAGTATCG
 GTGAGACTTCAATCAATATAGGTGGGTTTGATCTGGACATCAAAGGCTGGGCGGAGAGGATGTGCAC
 CTTTTTCGAAGTATCTCAACAGCAACCTCATGTGGTACGGACGCCCTTGCAGGAGATTTCTCCACC
 TGTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCCGAGCAGTACAAGATGTGCATGCACTCAA
 GGCCATGAAACGAGGATCCACCGGCCAGCTGGGCATGCTGGTCTTCAGGACAGGATAGAGGCTCAC
 CTTTCGCAACACAGAAACAGAAAGACAGTAGCAAAAACAGTGAACCTCCACAGAGAAGACATTCACATAAGAGC
 CACTTTTTCTTTCTTTTGCATTTACTGAAATGTGCTCAACAGAGAAGACATTCACATAAGAGCAGC
 ACAAAAGAAATTTGAGACTTTCGGTTCAGATGAGAAAGCTCTCCAGTCAAGAGAAGACATTCACATAAGAGCAGC
 AACAGAAATCAAAATCTCCGCTTTGCTGCAAAAGTAAACCAGTTGCACCTGTGAAGTGTCTGACA
 AAGCAGAAATGCTTGTGAGATTATAAGCCTAATGGTGTGGGACTTACATGGTGTTTACAATACACT
 GAGACCTGTTGTTTTGTGTGCTCATTGAAATATTCATGATTTAAGAGCAGTTTGTAAAAAAATTCAT
 TAGCATAGCATCAAAATGATGGCCATATCGAAGGACATGCCAAATGCTGATTTCTGACGGCTTATGAG
 AATGCTTAAATATCAGAAGGCGAGGAGAGAGATAGGCTTATTTATGATACATAGTAGATCATTAACTA
 AATAAAATGGACCAAGAAAGAAAGAAACATTAATATCGTGTCTATTTTCCCAAGATTAACCA
 AAAATTAATCTGCTTATCTTTTGGTTGTCTTTTAACTGTCTCCGTTTCTTTCTTTATTTAAAAAT
 GCACTTTTTTCCTTGTGAGTTATAGTCTGCTTATTTAAATACCACTTTCGAGCCTTACAGAGAG
 GCACAGTTTGGCCTACATTTTATATTTTAAAGAGATACCTTTGAGATGCAATATGAGACTTTCA
 GTTCAAAGCATCAAAATGATGGCCATATCGAAGGACATGCCAAATGCTGATTTCTGACGGCTGAT
 GTGAGGATTTGAGACATAGGGAAGGATGCTTTGTCTATACAGACATCAGATACCTTTCTCTGAA
 AAGCAAACTCACTCAGACTGGTGATATCGTAGTGAATTAAGAGTCAAGAACCACTTTTCTCCICA
 GAGTATGGGACGCTTTCTTACTGTTTAAATAAACCAAGTATACCGTGTGAACCAACCAATCTCT
 TTTCAAACAGGCTGCTCCTCGCTTCTGGCTTCTGGCTTCCATAAGAAAGAAATGGAGAAAAATATATAT
 ATATATATATTTTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTGTGCTACAT
 GTTATACACCCAGGCTGGAAAGTAACTGAATTTTAAATTAAGCAGTCTACATCAATCA
 CCAAGATGCTTTGTAAAAATGCAATTTTATACCATTTCAAACTATTTTAAATAAATACAGATTA
 ACATAGAGTGTGTTCTTCTCATCTGATGAAATAATTAGCCAGCCAGATCATGAGCTATGATCT
 TTTGAGTCTGCTTCTGTGTGCTCAGAGTAACTCATTTTAAAGCTTCAGAAAGCTTCAGC
 GTTGTGGTGTAAAAAATGATTTGATTTGCTAGGTAGTTTATGAAATTTAATTAACCA
 AGGCCATGAATGGAAGGTGGTATGCACAGCTAATAAATATGATTTGTGGATATGA

FIGURE 276

MMVVRGLLAWISRVVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVIQ
EWEEQHNRNYVSSLKRQIAQLKEELQERSEQLRNQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIES
ALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNKELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

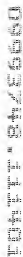


FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACCTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAACCCAGAGGGT
 ATCATCTCGTTTTGTGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTCTTTCTAAATGACCAAAT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCGTCTTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCTCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCCTTCTTTGTAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAGCTATTCACGAC
 TCAAAATATTTCTAAATATTTTTCTGACAGTATAGTGATAAATGTGGTCATGTGGTATTTG
 TAGTTATGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTGACGATCAGTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTTGTTGACCATTCTACAATTTGTAAAGTCCAATCTGTGCTAACCTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDNTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFWFVVTDP SKNHTLPAVEVQSAIRMKNRINNAFFLNDQTL
FLKIPSTLAPMPDPSVPIWIIIFGVFICIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGIIMMPS

FIGURE 279

AACTCAAACCTCTCTCTGCGGAAAACGCGGTGCTTGCTCCTCCCGAGTGCGCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCGCGTCTCTGGGGCCAAGGCTGGGTTTCCCT**ATGT**
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAATGCACCTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGTGA
 AGAACCACCTGATGTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACITCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTCCAAGAACAA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTACA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTATGACTTGATACACATATATTGGTATCAAAGGGGATAAAGCC
 AATTTGTCTGTTACATTTCCCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTCTCTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATTCAACTGTTAAATGACATTTTTATTTTTATGTCTC
 TCCTTAACATATGAGACACATCTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
 TTTGTCTG

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQVFVYHYIDFPQPMGRFKDRVSWDGNPERYDASILLWLKQFDDNGTYTCQ
VKNPPDVGVGIGIRLSVVHTVRFSEIHFLALAIQSACALMIIVIVVVLQFHYRKKRWAER
AHKVEIKSKEEERLNQEKKVSYLEDTD

FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCTCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTTCATGCTTCCTGTGATTC
ATCCAACACTTACCTTGCCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

Category	Sub-category	Value	Unit
Total	Population	100	%
	Area	100	%
Urban	Population	50	%
	Area	50	%
Rural	Population	50	%
	Area	50	%

FIGURE 282

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTAT
 TAASTTARKDIPVLPKWVGDLPNGRVCP

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTGTGCTGGTTAACAAGATAAAGTGGGAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCTGGGTGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAACCTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

284/330

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERITLGKVQRWSGVHTQTGGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

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FIGURE 285

GTCATGCCAGTGCTGCTCTGTGCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTGCGAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTGAATCTGCCTGGATGGAATGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACCTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCATGCCTACACCCCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAAPMGGPELAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

286/330

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAAATGGACTTGTAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACGAGCCACACATCCAGATTAAAGGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATGAAAAGCTC
 TGACAGAAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCAGGAACTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGTGACGTCAACGGAATCGTATCTCCTTCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCGTGTCGAGCAGCAAGAGATACATATGCGAGTTTACCATTCCC
 TAAATAGGTCCTTCTCCAATGTGTCTCCAAGCAAGATTTCATCATAACTTATAGGTTTCATGA
 TCCTTAAGATCAAGTAAAAATCATAATTTTTACTTTATAAAAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCGTCT
 AAACAGACTAAAATCTTCTCTCTAGTCTTCTCACTTGTACAAACCCAGTTTGTGTTTCAA
 AATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAAACTTTTAGCCTGTTGCTCATTCTGTCCATGCTGGCAATAATACC
 TTGTGAGCCCATACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTACATTT
 TCGTATATTTATTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGGAAAATGTCATACGTCTGTGCAATT
 TTTTATCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAGTTTAGACTTGGAGGGAAATGGGCTTTTGAAGCAACCAATTT
 AAATATATTTTGTCTTCAAATAAATAGTGTAAACATGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACCTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAAGCCTGAATTCGTATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

288/330

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSAQGK
WSDEACRSSKRYICEFTIPK

288/330

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCCAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCTGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCTGGCCAACCCCTCGGCACCCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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TGAAGGACCTTTCCAGGACCCCAAGGCCACACACTGGAAGTCTTGCACTGAAGGAGGCACCTCTTGGCTCCGCGGATCATGAAAGGAGGCTGCTGCTCTCCGCTCCCTCTCTGCGACAGGTGTGGCTGGTACCGCGCTTGGCCCGCTCTCAGTTCGCGACGAGACCCGAGCCCTTCAGAACAGACAGCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAGGCGAGGAGGAAGGCGGGTAGGAGGAAGAAAGCGTGGCTGATGGCCAGCGAGGACGCTCCGCAAGGAGACTTCAAACCTCGGAATTCAGCTGCTGCGAAGAGATTCATGAGGCACGATGCAACATGGTCTTCTCTCCATTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCGGACTGAACCCAGATCAAGAGAGGGCTCCACTGGAGGCCCTGAAGCCCCCAAGCCCGGGCTCTGCTCTCTCTCTTTAAGGACTCAGAGAGACCTCTCCGCAACCTGGAAGTGGGCTCTCAGGGGAGTTTGCCTTCATCCACAAGGACTTTGATGTCAAAGAGACTTTCTCAATTTATCCAAAGAGGTATTTGATACAGAGTCGCTGCCTATGAATTTCCGAATGCTCTCAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAAATCCCAAACCTGTTTGATGAGATTAATCTGAAACAAATTAATTTCTGTGGATTACATCTTGTTCAAAGGGAATAAGTTGTGACCCCATTTGACCCTGTCTCTACCAGAGTCGACACTTTCCACTGGACAGGTACAAGACCATTAAGGTGCCATGATGTACGGTACGGGCAAGTTTGCCTCCACCTTTGACAAGAAATTTTGGTGTGATGTCTCAAACCTGCCCTACCAAGGAATGCCACCATGCTGGTGGCTCTCATGGAGAAATGGTGGACCACTCGCCCTTGAAGACTACCTGACCAAGACTTGGTGGAGACA TGGCTCAGAAACATGAAACCAGAAACATGGAAGTTTCTTTCCGAAGTTCAAAGCTAGATCA GAAGTATGAGACATGAGCTGCTTAGGACAGTGGGAATCAGAAGAAATCTCTCACCTTTGCTGACCTTAGTGACTCTCAGTACTGTGAAGAAATCTCCAAGTATCAGGTTTTCAGGAACAGAGTGAA GTTGTATGAA GTTGTATGAAAGGGGCACTGAGGCAAGTGGGAGGAATCTTGTTCAGAAATTAC TGCTTATTTCCATGCTCTCTGTCATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG AAACCTCTGGAATGCTCTTCTTCTTGGCAGGGTGGTGAATCCGACTCTCCTATTAATTCAGG ACATGCTAATGCACTCTGCTGCTGATAGATGCTGAAATCTGAGGATCAACACACACAGGTA TACCAGCAATGGATGGCAGGGGAGTAGTGTCTCTTTGTCTTAACTAGTTTGGGTGTTCTT AAATAAATACAGTAGTCCCCACTATCTGAGGGGATACATTTCAAAGACCCCCAGCAGATGCTGAACCGGTGGACAGTGCTGCAACCTATATATATTTTTCTCACATACATACATCATGATGAATAAGTTTAATTTATAAATTAGGCACAGTAGAGATTAACAAATATAACAACTAAGTAAATAGTACTGAAAGCAAGCACTGCAATACCATAACAGTCAAAGTGATTATGAGAGGGCTA CTAAGTGAATCACTGGGCGAGGACATAGACAGCTGTGGACACTTGGGCAAGGGGAGAAATTCACATCTGGGTGGGACAGAGCAGGACATGCAAGATTCCATCCCACTACAGAATTGGCATTC TGCTTAAGACTTTTAGATTGTTTATCTTGGAAATTTTCAATTAAGTGTTTTGGACCATGGTGCATATGTTTAACTAGTACTATTTTAAAAAAA

FIGURE 292

MKVVPSLLLSVLLAQVWLVPGLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGE
EEKAWLMASRQQLAKETSNFGFSLLRKISMRHDGNMVFSFPGMSLAMTGLMLGATGPTETQI
KRGHLHLQALKPTKPGLLPSLFKGLRETLSRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGI PKLFDEINPETKLILVDYILFKGKWLTPFDP
VFTEVDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL
ALEDYLTDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRI FSPFADLSELSA
TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIEETSGMLLF
LGRVVNPTLL

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC
TGTCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGCTCCTGAGTCCC
GAGCCCACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAATCACCAGGTGCTCCTGGGACCGAGGAAGACCAAGACCACA
TCTACCACCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAATAAACCCACGAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 294

MRRLLVTSLVVLLWEAGAVPAKVPKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPCLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCACTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTCTG
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGACCTGGGCATCTGGCAGCTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAACAGCATCTTATTACTCACCCATATGCCAGCGGAATTCAGTGCGGGATT
TGTTCACTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTTGTCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTGTATTGGAGTGGATATGGAACATCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG
GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGLI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCTGCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCGG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAACTGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT
 TCTGAAGCAAAGAAAGGATCAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTCT
 GGATCGAACCATAGATGAACATGATGCCATCATTTAAGGAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCATCAATTAATTTTGGTTTTATTAATAGTTTTAAACAATATTTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTTCTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCTATCTTTTTTTTTGGCT
 GGGGTGGGGCATTTGGTCACATATGACCAGTAATTGAAAGACGTCACTCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTCACAGCACTCAGGATTTTGGGTATCTTTGT
 AGCTCACATAAAGAACCTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

MGLGARGAWAALLLGTIQLVALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
 TNETSNSTVKPPTSVASDSSNTTVTMTKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
 TSQISTSTMVTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTGLVLSILYIG
 CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGGCGACCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCTGCTGGCGCTTTCCGTGCTGCTGCTGGC
 GCAGCTGTGAGCGCGCCCAAGAATTTCAGGATGTGAGATGTAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAATATGAAGAAAGAGCTCTGTCACAATCAAGGTTACCATTTATAATTTATCTCTCCA
 TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAATGCACAGATGTGCTAGCCCGCTCCCGAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCCG
 CATGTTGTCTCAGCTAATTTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAACTCCTGTTGATTTCACCAACT
 GTTGTGGAAGATTCAAACCTGGAAGCAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAATATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTACCCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTGTGTTGTTGTTGTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGT
 AACAACTTTTTCAAGTCACCTTTACTAAACAACTTTGTAAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATTTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCAGTACTGTATTATCTGGGTATCTGCTGTGCTGCACCTTCATGGTAAACGGGAT
 CTAAATGCCTGGTGGCTTTTCAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTGTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGGTCTTACTCATCTTAGTACCTTTAAGGACAACTCCTAAGGACTTGGACACT
 TGCAATAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTTATTGGATAACTGGCTTTTT
 TCTTCTATGCTCTTCTTGAATGTAACAATAAAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS
QKDCDCLHVVEFMPVRGPDVEAYCLRCECKYEERSVTIKVTII IYLSILG
LLLYMVYLT
LVEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYA
QQRWKLQVQEQ
RKSVFDRHVVL

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTGCTGCTGCTGCCAAGGCCCTTCTGTCCCGCGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCGAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAAGTGTGTTTGGCCCAAATTCACAACTACAAGGCAGAAGTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGFRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGCATGTTTTTGCCCACTGAAACTCATCTCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTACAGCTCTGATGGGATGTGTTTTCCAGAGCAGAGAAGACAAATGTATATTCAAGAT
AGACTGGACTCTGTCAACAGGAGAGCAGCCAAAGGACGAATATGTCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCTGACACTTGTATGGGGGACATCTTATGC
AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG
AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
GGAGATTGTATTTGTTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAAGAAAACCATTTGTCTGCATGTGAGCCCGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCTCTGTCTTGGGTGGTAAATCAGTTGGTGATCATTTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACATTTACTCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCCTGTGTGTGTCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC
CCAGCTGTCTCCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
GGATCAGACCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCAATCA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLRMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRESGGNYTCSIHLGNLVFKKTIIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTV
LVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIIVREVIEEEEPEKSEATYMTMHPVWPSLR
SDRNN SLEKKS GGGMPKTQQAF

304/330

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
GGATGAAGATGGATACATCACCTTAAATATTTAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTGGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
AGAACAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

MQDEGDYITLNIKTRKPAIVSVGPASSSWVRVMAILLILLICVGMVVLVALGIWSVMQRNYL
QDENENRTGTLLQQLAKRCQYVVKQSELKGTFKGHKCSPCD TNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARHTLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCCTGCTCCGCTGCCAGTCTCGCCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
GCCCCGGCAAACG CAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**CATG**CGCGCGGCTATCGCCAGCTCGCTCATCCGT CAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGCTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGCTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGCGGATGGAACCATTGATGGCACC AAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTGTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCAGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGT CAGTGACATTTACCAAACAAACAG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCTTCTGACATTGGCAGTG
 CCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCTGTAGATTAC
 AAGAGTGGATTGTCAGGAGTGTGCCCCAAATACAGTGAAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTCAATAGGAGGCCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAAGTGGCTGCT
 GTGGAGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG
 CGCGCTCCGGGCGCTGCCGGTTTGGGGGTGTCTCTCCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCCGCAGCCCGGGGGCAGCCGGCCGGTGTGG
 CGCAGCGGCGGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCGCGCGGCGGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAATGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCACAGAGGATACCACTCCTTCACCCACTTCAACCTGATCCCT
 GTGGGCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCGTTTAAAGAGTGTGTCT
 TTGAGAATTACTACGTCCTGTACGCCTCTGCTCTTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGGCCAGGTGATGAAGGGAAACCGAGTTAAGAAGACAA
 GGCAGCTGCCCACTTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGGCCTCCCTTCCAGTCCCCCTGCCCTCGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRFVSAQRRVCPRGKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLAQNPDSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTAAAAACAGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAACACAGTCAACAAGAGTAAGACAACATAG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWD RPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHDPD GALDGT KDDSTNSTL FNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYVYIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETV PKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

GGGAGGAGGAATTGACCATGTAAGAGGAGACTTTTTTTTTTGTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAA
GAAGGATGCAGGAGCGAGCTTTCTCCTGGAAACCGAACGCAATGGATAAATCTGATTGTGCAAGAGAGAGGAAGA
ACGAAGCTTTTCTTGTGAGCCCTGGATCTTAAACACAAATGTGTATATGTGACACACAGGGAGCATTCAGAATG
AAATAAACCAAGCTTAGACCCGCGGGGTGTGGTGTCTTGACATAATAATAATCTTAAAGACAGCTGTCTCCC
CTCCCAACCCCCAAAAAAAGAGGATGTGAATTAAGAACCCAGGATTCACAAAGAAAAAGATGTCTCATTT
TTCTCTATAAAGGAGAAAGTAGGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
AGAACTGGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCCAACAGAGGAGAGGAAATTAATATACATCTGC
AAAGAAATTTAGAGAGAAAAGTTGACCGCGGCAGATTGAGGCATGTATTGGGGAGAGAAACACGACGACGA
CAGTTGGATTTGTGCGTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACTCCTTT
TTTTTAAATTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAACCACTGGATTTCCATCT
GGATGTTGCTGTGACTAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAAATTATGAATG
TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTGACCCCT
GCTTGTGGTGTGCTGTGCTCTTCAACTTCTTGTGGTGGTGGTCTGTTGCGGGCTCAGACCTGCCTCTGTGT
GCTCCTGCGACCAACAGTTGACAGAGGTTGATTTGTTCGGAAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
ACCAACACACGGCTGCTGACGCTCCATGAGAACCAATCCAGATCATCAAAGTCAAGCCTTCAAGCATGTAG
CGGATTTGGAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGCTTCAATGGTCTGGCGA
ACCTCAACACTCTGGAATCTTTGACAAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAA
CTGAAGGAGCTCTGGTTGCGAAACAACCCCAATTGAAAGATACCTCTTATGTCTTTAACAGAATTCCTCTT
GCGCGACTAGACTTAGGGGAATTGAAAAGCTTTCTATACATCTCAGAAGTGCCCTTGAAGCTCTGCTCCAAT
TGAGGATTTTGAACCTTGCCATGTGCAACTCTCGGGAATCCCTAACTCACCCGCTCATAAACTAGATGAG
CTGGAGCTTTTCTGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGSGTTTGTATGCACCTTCAAAACT
GTGGATGATACAGTCCCAGATTCAAGTGATTGAACCGAATGCTTTGACAACTTCAAGTCACTAGTGGAGATCA
ACCTGCGCACACAATAATCTAACATTAATGCTCATGACCTCTTCACTGCTTGCATCATCTAGACGGATACAT
TTACATCACAACCTTGAAGCTGTAAGCTGTACATCTGTGGCTCAGCTGGTGACATAAAAGACATGCCCCCT
GACACAGCTTGTGTGCGCGGTGTAACCTCTCCCAATCTAAGGGGAGTGATTTGGAGAGCTCGACCGACA
ATTACTTACATGCTATGTGCGCGGTGATTGTGGAGCCCTGACAGCTCAATGTCACTGAAGGCATGGCAGCT
GAGCTGAAATGTGCGGCTCCACATCCCTGACATCTGTATCTTGGAATTACTCCAATGGAACAGTCATGACACA
TGGGGCGTACAAAGTGGCGATAGCTGTGCTCAGTGATGGTACGTTAAATTTCAACAGCTGTAAGTTGCAAGTCA
CAGGCATGTACACATGTATGGTGAACTCCGTTGGGATACACTGCTTCAAGACCCCTGAAGTCTTATGCA
GCAACCACTACTCTTTCTTACTTTTCAACCGTGCAAGTAGACATTTGAACCGCTCAGGATGAGGCAG
GACCACAGATAACAATGTGGTCCCCTCCAGTGGTGCAGCTGGGAGACCACCAATGTGACCACCTCTCTCACAC
CACAGAGCAAGGTCGACAGGAAAAGCTTACCATCCCACTGACTGATATAAACAGTGGGATCCCGAAGATT
GATGAGGTCATGAAGACTACCAAAATCATCATTTGGGTGTTTTGGGCCATCACACATCAGGCTGAGTATGCT
GGTCATTTCTACAAGTGAAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAGAGCTGTGGAATTA
TTAATGTGATGATGAGATTTACGGGAGACACACCATGGAAGCGCACTGCCATGCCGTGCTGTGAGCATGAG
CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACACAGTTAACACAATAAATCAATACA
CAGTTCAGTGCATGAACGTTATTGATCCGAATGAATCTTAAGACAAATGTACAAGAGACTCAATTAAGACA
TTTACAGAGTTACAAAAAACAAACAAATCAAAAAAAGACAGTTTATTAATAAATGACACAAATGACTGGGCTAA
ATCTACTGTTTCAAAAAGTGCTTTACAAAAAACAAAAAGAAAGAAATTTATTATTAAAAATCTTATGT
TGATCTTAAGCAGCAAAAAA

FIGURE 314

MLNKM TLHPQQIMIGPRFNALFDPLLVVLLALQLLVVAGLVRAQTCPSCSCSNQFSKVIC
 VRKNLREVDPDGISTNTRLNLHENQIQIIKVN SFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNFTNVTQDTGMYTCMVSNVSGN
 TTASATLNVTAAATTFFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKTFFTPVTDINSIGPIGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
 HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTTVTNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

GC GCGCGGGAGCCCATCTGCCCCACAGGGGCACGGGGCGCGGGGCCGGCTCCGCCCCGCACAT
GGCTGTCAGCCACCTCGCGCGCACCCGAGCGCGCGCCAGCTCGCCCGAGGTCGCTCGGGA
GGCGCCGGCGCGCCGCCGAGCAACAGCAAGCTGAGCGGGGAAGCGCCGCGCTCGGGGATC
GGGATGTCCTCTCTCTCTCTCTCTGCTAGTTTCTCTACTATGTTGAACCTTGGGGATCA
CCTGAGATCAAGAGATGGCAGAGGAAAGGTCAATTGCCCTGCCACCATCACTCACTGGGG
TTCCAGAAAAAGACACTCTGGATATTGAATGGTGCTCACCATAATGAAGGAAACAAAAA
GTGGTGATCACTTACTCCAGTCGTATGTCATACAACTGACTGAGGAACAGAGGGCCCC
AGTGGCCCTTTGTTCCAATTCTCTGGCAGGAGATGCCTCTTGCAGATTGAACCTCTGAAGC
CCAGTGTAGAGGGCCGCTACACTCTTAAGGTAAAGATTACGGGCGCTACGTGTGGAGCCAT
GTCTATCTTAAAGCTCTTAGTAGACCATCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCACTGTGAGTCACTCCCTGGCAGAGCCCATTTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGATTGAAGCTCTGCCCTCCAAATCTAGGATT
GACTCAACACCGCTGGACGAGTTCTGCTGCAGGAATCTACCATCTGCTACTCTGGACTGTA
CCAGTGCACAGCCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACGTGACAGT
ATGTACAAGAAGCTCGGCATGTTGTGCAGGACGAGTGCAGCCAGTAGTGCGCTGGAGCCCTGCTG
ATTTTCTCTTGGTGTGGCTGCTAATCTCCGAAGGAAGAACAAAGATATGAGGAAGAGA
GAGACCTAATTGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAACCCAGCT
CCTCTCTCCTAGCCTCTCGGAGCTCAGCCTCTGGTGTCTTCTCCTCACTCGCTCCACAGAAAT
AGTGCTCAGCGAGCCAGCGGACATGTCAACTCAGCAGCAACCCAGCAGGGCTGGCCAC
CCAGGCATACAGCTGTGTTGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAGATCCACCAT
CTAATCTGACCAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGAGCAGGCTTCCAA
ACGGTCTGAATTAACAATTGCACTTGACTCCACGCTTTCCTAGAGTCAAGGTCCTTTGGACTC
TTCTCGTCACTTGAGCTCAAGTCAACAGCCACACAAACAGATGAGAGGTCATTAAGTAGTA
GTGAGCATTCGACCGGAACGATTAGATGACATTTTCTTATACATAACCAACAGCAAA
AGGATGTAAGCTGATTATCTGTAAAAGGCATCTTATTGTGCTTTAGACAGAGTAAGGG
AAGAGCGAGGTCCAAATCTATTTTTGACACGAGCTGTGGTGAGAAGTTGGGGAAGGTG
AGGTGAATATACCTAAACTTTAATGTGGGATATTTGTATCAGTGGCTTGATTCACAAAT
TTCAAGAGGAAATGGGATGCTGTTGTAATTTCTATGCAATTTCTGCAAACTTATGGATT
ATTAGTTATTACAGAGTCAAGCAGAACCCACAGCTTATTACACTTCTACACATGTAT
TGAGCTAACCATTTCAAGAAATCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TCTATTGTCTATAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAA
AGAGTGAATGAGTTTCTCCCATCTATACTAATCTCACTATTGTGATTGAGCCAAAAATAC
TATGAAGGAGACAAAAATTTGTGCAAAAGGATTGTGAAGAGCTTTCCATCTCTATGATGTT
ATGAGGATTGTGCAACACATTAGAATATATATAATGAGCAATTGTGGATTTCCTCCATCAAT
CAGATGCCCTCAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATACAACATGTCTATT
TCCACAGCTCTTTAGAAGAAATTTCTTCAGAAAAAGGATCTAGGAATGCTGAAGATTA
CATCAACATCACTTATAGTCTCTTCTTCTTGAGAAATGTGAACCAAGAAATGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGCA
TGGTGCCAGGCACCTGTAGGAAATCCAGAGGTTGGAGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGCACTCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNLTTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFAQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLLCFVLLCGVVDFARSLSTTPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARYVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSPNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSFTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAAACACCAAGAAGATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCAGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCACACCTGCTGGAGTCTACTTGAAAACTGTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTCTGCTATTCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCAC TGGTTGTTCCCTGTGTCATTCA
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGCCATGGGTCCCATTC
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCATGCTTCTTTACCCCTCACAATCCTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAAC TGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAGG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTATT
 TCCACCACACTCGCCAGCTCACCCATCATCCCTTTCCCTTGGTGCCTCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCTGCTAATAAAGACAACATAA
 CTCCAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFAQRLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLSQVSGAQGGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRREFLLFRRAFKQLDVEEAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTC AAGGATCA
TCAGGAGCCAAACCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTG CAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTCTGAATAAATTCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACCATGTTGGGGGCCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTTGGATCACACTATTTTCGAC
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGCAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCCTGTCCCGAGGAACGAGATCCCCCTAATTCACCTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCCGATGACCCCGGCCCGGCCCTCCTGTTACAGGAGCTCCCAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCA LCSVCSMSVL RAYPNAS PLLGSSWGGLIHLYTATARN SYHLQIHKN GHVD
 GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENC RFQHQ TLENGY
 D VYHSPQYHFLVSLGRAKRAFLPGMNPPPY SQFLSRRNEIPLIH FNTPIPRRHTRSAEDDSE
 RDPLNLVKPRARMTFAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
 KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGGATG
 GGCTGTCTCTGGGGTCTGGGCTCTGCCCTTTTCTTCTTCTGTGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCCGGGCCACGCGCTCTGGAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCCTCAT
 GGTCCCCGGGATCTGATGTCACTCTCTCGTGAAGCCCTGGTGACTGTCAAAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACACTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCACGGAAGGGGTGAAGGCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGCCACCAAGAGAGTCACTGACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAAGAGAAGTGACAGCACCCGGGCCACGACCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGACAGTGGGCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCCCTCGAAGCCGCCCTCAAGAACTTCACCC
 CTTGAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACGTGAGTGCAGGTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGTTCCCCGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACTCACGCCACCGCGCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGAGGCTA
 ACGGACATCAGTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCAGACACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGTCCTTGGACTCACCTTG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
 TTAAAAATCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRADTAMTTDDTEVPAMTLAPGHAALETQTLSEA
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQTIITGSDPEEAFDITLCTDDSEEAKTLTMDILTALHTSTEAKGLSSESSASSDGHPHV
 ITPSRASESSASSDGHPHVITPSRASESSASSDGHPHVITPSWSPGSDVTLLEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVETPSY
 VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAAALKNFTPSETPTMDIATKGFPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCTGCGGAGACCCCGCGCGGATTGCGCGGTCTCTCCGCGG
 GCGGAGCAGAGCTGTCTCTGCGACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCTCGAGGCCA
 GAGAGAAATCTCATCTGTGTCAGCCTCTTAAAGCAAATTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTCTCGGGGAGAGGGGAG
 CTTGACTTACACTTTGGTAAATATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAAT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTGCTGTTCAAC
 AAAAAACATATCAGGGGCAAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAATTTTCAACAAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTTCAAAGCCCAACCGATATCTCATGGAGAGACACATTTTCT
 CAGAAGTTTGGATCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCATGTCACTTCTC
 AGCCTCCACGACCTCATTTTCTACAGTTTTTACACGGGCTCGGGTACACTCCAAGCAATG
 GCTACACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTCTCTCCAGGGCAGTGTCCAGAAAACTCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGGTGATAGGCC
 TCGTCTCTCGGGTGAATCCTTTCCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGGCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCTTCTGCTTTTCTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGCTCTC
 CTGGGTTCAAGCGATTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTACCATTGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCTCGGCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCACTGGCTTTTATGCAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATCTTGGTTCAGATAAAATCAAC
 GTTTTATCAATTTCTAATGGATTGCTTTCTTTTATATGGATTCTTTTAAACTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLKSGIRGNPEVYTSTQED
CINSCCSTKNISGDKACNLMI FDT RKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESTMTNKATASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFVLVIGLVLLGRILSES LRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGCGCCAGAAATGCGGGTCTTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCTTGCAGTGCACCTACAGGGAAGAGCTGAGGGACACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGCTGCTGGCACCATCTATGCAGAAAGGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGACCCCTGTGGA
 ACCTCACCCGTCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTGTGTCGTCTTCCAGGACCCCTGCTGTCCTCCCTCCCCCTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCTGACAGCCCAAGGCAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGCAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCCAGCGACCTCTCTCTGACAGGGAGCTCCCGCCCCCATGCGAG
 TGGACTCCACCTCAGCAGAGGACACCAAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTGCTGCTGAGCCTTCTGTGAG
 CGCAGGCCTGATCGCCTTCTGACGCCACCTGCTCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAACTTCTGGCTCTCAGCTTGAAGTCCGGAGGAAAAGGAAGCC
 CCTTCCAGGCCCTCAGGGGGACGCTGATCTCGATGCCTCCCTCCACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTGTCTCAGCGTAGGGCAGGAGCCCTCTGGCCACGGCCAGCAGT
 GAAGCAGTATGGCTGGATCAGCACCATTCCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTTCCAGGCTCTCTCTTGCATGTTCCA
 GCTGACCTAGAACCGTTTGTGAGCCCTGGAGCCACAGAGCGTGGCCTTGTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 CAGGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCCAGTGTGCGACCCCTGCCTTCTCTCCACTCCAGACCCCAAGCTTGTCTTCCCTCCC
 TGGCGTCTCTCAGACTTAGTCCCACGGTCTCTGCTCAGCTGGTGTGAGGAGGAGCAGTGT
 GGGGTGAGACTGGGATCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTCAGGAAGGCT
 GTGAAAAACGTGATTTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCAACAATGCCAGTGACTGTCGCACTTGAGTTTGAAGGGCCAGTGGGCGTG
 ATGAACGCTCACACCCCTCAGCTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACTGCCC
 CAATAGATCTGCTCTGCTCTGCGACACAGATCCACGTTGGGGATCTCCCTGAGGCCCTGTAAAG
 TCCAGGCCTTGGTCAGGTGAGGTGCACATTGACAGGATAAGCCAGGACCGGCAGGAAGTGG
 TTGCTTTTNCCTTTGGCCCTCCCTGGNCCATGCCTTCTGGCTTTGGAAAAAATGATGAAGA
 AAACTTTGGCTCCTTCTGTCTGGAAGGGTTACTTGCCATATGGGTTCTGGTGGCTAGAGA
 AAAAGTAGAAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGATAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTTGGAGAAGGGGTGGGGGGTGGTGGTAAAGTA
 GCACAACACTACTATTTTTTTCTTTTCCATTATTATGTTTTTAAAGACAGAATCTCGTGCT
 GCTGCCAGGCTGGAGTGCAGTGGCAGCATGCAAACTCCGCTCTGGGTTCAAGTGATT
 CTTCTGCTCTCAGCCTCCGAGTAGCTGGGATTACAGGCACGACACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAATCTGTGAC
 CTCAAATGAGCCTCCTGCTTCTCAGTCTCCAAATTTGCCGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTAAAAAGTGAATTAAGAGTTGTTTCAATATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAAAGTGTCAACCATAGCTCACCAGATCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTGTACTTCTTCCACTCTTTTCTTCTTCACATAATTTGCCGGTGTCTCT
 TTTACAGAGCAATTATCTGTATATACAACCTTGTATCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATCCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

MRLVLVLWGCLLLPGYEALEGPEEISGFEGDTVSLQCTYREELDRHKRYWCRKGGLFSRCS
 GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDQAGEYWCVEKRGPDSELLISLFFV
 FPGPCPPSPSPPTTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAAATTAQKGTGAEPPLPG
 TSQYGHERTSQYTGTSHPATSPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
 LAPVLVLLSLLSAAGLIAFCSHLLWRKEAQATETQRNEKFWLSRTAAEKEAPSPAQEGD
 VISMPLHTSEELGFSKFVSA

amino acids 13-128